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# OM protein - protein search, using sw model

Run on: December 20, 2004, 14:06:51 ; Search time 153 Seconds  
(without alignments)  
236.808 Million cell updates/sec

Title: US-10-630-590-288

Perfect score: 528  
Sequence: 1 PSELKGRFHTLRKSRGRF.....IGASVDELRCRGVLPFPDP 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528	100.0	101	8	AD153645
2	528	100.0	101	8	AD153736
3	528	100.0	103	7	AD153735
4	528	100.0	104	8	AD153477
5	528	100.0	104	8	AD153568
6	528	100.0	104	8	AD153568
7	528	100.0	108	8	AD153781
8	528	100.0	263	5	AD153188
9	515	97.5	99	8	AD153658
10	515	97.5	99	8	AD153749
11	514	97.3	740	5	AAU87919
12	485	91.9	94	8	AD153657
13	485	91.9	94	8	AD153748
14	466	86.4	88	8	AD153654
15	466	86.4	88	8	AD153745
16	452	85.6	88	8	AD153655
17	452	85.6	88	8	AD153746
18	436	82.6	85	8	AD153652
19	428	81.1	86	5	AAU87854
20	428	81.1	86	5	AAU87854
21	418	79.2	887	5	AAU87932
22	418	79.2	1112	3	AAU87932
23	418	79.2	1161	3	AAU87932
24	418	79.2	1216	7	AD153657
25	418	79.2	1277	3	AAU87932

26	415	78.6	81	8	AD153656	AD153656 Human MAG
27	415	78.6	81	8	AD153747	AD153747 Human MAG
28	399	75.6	78	8	AD153653	AD153653 Human MAG
29	399	75.6	78	8	AD153744	AD153744 Human MAG
30	391	74.1	76	8	AD153651	AD153651 Human MAG
31	391	74.1	76	8	AD153742	AD153742 Human MAG
32	386	73.1	104	8	AD153661	AD153661 Human MAG
33	386	73.1	104	8	AD153662	AD153662 Human MAG
34	379	71.8	103	7	AD153667	AD153667 Human MAG
35	377	71.4	104	8	AD153650	AD153650 Human MAG
36	367	69.5	72	8	AD153658	AD153658 Human MAG
37	367	69.5	72	8	AD153659	AD153659 Human MAG
38	365	69.1	72	8	AD153660	AD153660 Human MAG
39	365	69.1	72	8	AD153661	AD153661 Human MAG
40	365	69.1	72	8	AD153662	AD153662 Human MAG
41	365	69.1	72	8	AD153663	AD153663 Human MAG
42	364	68.9	72	8	AD153664	AD153664 Human MAG
43	364	68.9	72	8	AD153665	AD153665 Human MAG
44	364	68.9	72	8	AD153666	AD153666 Human MAG
45	364	68.9	72	8	AD153667	AD153667 Human MAG

## ALIGNMENTS

RESULT 1  
AD153645  
ID AD153645 standard; protein; 101 AA.

AC AD153645;

DT 22-APR-2004 (first entry)

DE Human MAG1 1 PDZ domain in pCEX-3X.

KW Human; PDZ domain; postsynaptic density-disc-large-20-1; HPV infection;

KM E6 protein; cervical cancer; cytoskeletal.

OS Homo sapiens.

OS Synthetic.

PN US2004018487-A1.

PD 29-JAN-2004.

PF 29-JUL-2003; 2003US-00630590.

PR 10-NOV-2000; 2000US-00710059.

PR 16-FEB-2001; 2001US-0269523P.

PR 03-AUG-2001; 2001US-0309841P.

PR 19-FEB-2002; 2002US-0080273.

PR 25-FEB-2002; 2002US-0360061P.

PR 02-AUG-2002; 2002MO-US024655.

PR 09-SEP-2002; 2002US-0409298P.

PR 27-FEB-2003; 2003US-0450464P.

XX (LUPS/) LU P S.

XX (SCHW/) SCHWEIZER J.

XX (DIAZ/) DIAZ-SARMIENTO C S.

XX (BELM/) BELMARES M P.

XX LU PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;

XX WPI; 2004-122015/12.

XX DR

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RESULT 1  
AD153645  
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PR 03-AUG-2001; 2001US-0309841P.

PR 19-FEB-2002; 2002US-0080273.

PR 25-FEB-2002; 2002US-0360061P.

PR 02-AUG-2002; 2002MO-US024655.

PR 09-SEP-2002; 2002US-0409298P.

PR 27-FEB-2003; 2003US-0450464P.

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RESULT 1  
AD153645  
ID AD153645 standard; protein; 101 AA.

AC AD153645;

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KW Human; PDZ domain; postsynaptic density-disc-large-20-1; HPV infection;

KM E6 protein; cervical cancer; cytoskeletal.

OS Homo sapiens.

OS Synthetic.

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PF 29-JUL-2003; 2003US-00630590.

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PR 16-FEB-2001; 2001US-0269523P.

PR 03-AUG-2001; 2001US-0309841P.

PR 19-FEB-2002; 2002US-0080273.

PR 25-FEB-2002; 2002US-0360061P.

PR 02-AUG-2002; 2002MO-US024655.

PR 09-SEP-2002; 2002US-0409298P.

PR 27-FEB-2003; 2003US-0450464P.

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XX (BELM/) BELMARES M P.

XX LU PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;

XX WPI; 2004-122015/12.

XX DR

CC sample with a PDZ domain polypeptide (postsynaptic density, disc-large,  
 CC ZO-1) and detecting any binding of the oncogenic HPV E6 protein in the  
 CC sample to the PDZ domain polypeptide. Also included are a system for  
 CC detecting the presence of an oncogenic HPV E6 polypeptide in a sample  
 CC (comprising a first and a second binding partner for an oncogenic HPV E6  
 CC polypeptide, where the first binding partner is a PDZ domain protein and  
 CC at least one of the binding partners is attached to a solid support, the  
 CC second binding partner being an anti-E6 antibody), determining if a  
 CC subject is infected with an oncogenic strain of HPV and a kit for testing  
 CC for the presence of oncogenic HPV E6 protein (the kit comprising first  
 CC and second binding partners for the oncogenic HPV E6 protein, where the  
 CC first binding partner is a PDZ domain protein). In the method of  
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 CC protein in a sample, the PDZ domain polypeptide comprises the amino acids  
 CC sequence of human Magi-1 PDZ domain 2. The PDZ domain peptide binds to  
 CC HPV E6 protein encoded by HPV strains 16, 18 and 45. The sample is  
 CC contacted with multiple PDZ domain polypeptides. The PDZ protein is a  
 CC fusion protein with GST (glutathione-S-transferase). The method is a  
 CC performed as part of a test for cervical cancer. The method is useful for  
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 CC protein in a sample thereby detecting HPV infection and possible risk of  
 CC cervical cancer. The present sequence is a human PDZ domain in the  
 CC context of its expression as a GST fusion protein.

XX SQ Sequence 101 AA;

Query Match 100.0%; Score 528; DB 8; Length 101;

Best Local Similarity 100.0%; Pred. No. 4.5e-60; Indels 0; Gaps 0;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTHTLKRSRGFGFTVVGDEPDEFLOIKSLVLDGPALDGMKMTGDIYSV 60

Db 1 PSELKGFHTHTLKRSRGFGFTVVGDEPDEFLOIKSLVLDGPALDGMKMTGDIYSV 60

QY 61 NDTCVLGHHTAQQVVKIPQSIPIGASVDLELCRGYPLPDPD 101

Db 61 NDTCVLGHHTAQQVVKIPQSIPIGASVDLELCRGYPLPDPD 101

RESULT 2

ADM33736 ADM33736 standard; protein; 101 AA.

AC ADM33736;

DT 03-JUN-2004 (first entry)

XX Human PDZ domain #2.

XX human papillomavirus; HPV; PDZ domain; HPV E6; cervical cancer;

KW Magi-1 PDZ domain 2; human.

XX Homo sapiens.

PN WO2004022006-A2.

XX 18-MAR-2004.

PF 09-SEP-2003; 2003WO-US028508.

XX 09-SEP-2002; 2002US-0409298P.

PR 27-FEB-2003; 2003US-0450464P.

PR 25-JUL-2003; 2003US-0490094P.

PR 29-JUL-2003; 2003US-00630590.

XX (ARBO-) ARBOR VITA CORP.

XX La PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;

XX WPI; 2004-248368/23.

XX Determining if a human subject is infected with an oncogenic strain of

XX human papillomavirus (HPV) by detecting the presence of any oncogenic HPV

PT E6 protein bound to the PDZ domain polypeptide using an HPV E6 binding

XX partner.

PS Example 4; SEQ ID NO 288; 234pp; English.

XX The invention relates to a method of determining if a human subject is

CC infected with an oncogenic strain of human papillomavirus (HPV).

CC Determining if a human subject is infected with an oncogenic strain of

CC human papillomavirus (HPV) comprises: (1) contacting a sample obtained

CC from the subject with a PDZ domain polypeptide bound to a solid support;

CC and (2) detecting the presence of any oncogenic HPV E6 protein bound to

CC the PDZ domain polypeptide using an HPV E6 binding partner, where the

CC presence of oncogenic HPV E6 protein indicates that the subject is

CC infected with an oncogenic strain of HPV. The method is performed in

CC conjunction with histological analysis of the sample as part of a test

CC for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ

CC domain polypeptide binds to HPV E6 protein encoded by HPV strains 16, 18

CC or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is

CC directly or indirectly bound to the solid support. The PDZ binding

CC partner is a labelled antibody that binds to the oncogenic HPV E6

CC polypeptide. The sample is a cervical scrape, biopsy or lavage. The

CC present sequence represents a human PDZ domain used in the method of the

XX SQ Sequence 101 AA;

Query Match 100.0%; Score 528; DB 8; Length 101;

Best Local Similarity 100.0%; Pred. No. 4.5e-60; Indels 0; Gaps 0;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTHTLKRSRGFGFTVVGDEPDEFLOIKSLVLDGPALDGMKMTGDIYSV 60

Db 1 PSELKGFHTHTLKRSRGFGFTVVGDEPDEFLOIKSLVLDGPALDGMKMTGDIYSV 60

QY 61 NDTCVLGHHTAQQVVKIPQSIPIGASVDLELCRGYPLPDPD 101

Db 61 NDTCVLGHHTAQQVVKIPQSIPIGASVDLELCRGYPLPDPD 101

RESULT 3

ADD12353 ADD12353 standard; protein; 103 AA.

AC ADD12353;

DT 01-JAN-2004 (first entry)

XX PDZ ligand (PL) protein #16.

XX modulator; PDZ; post-synaptic density protein 95; PSD95;

KW Drosophila large disc protein; Zonula Occludin 1 protein; ZO-1;

KW PDZ ligand; PL; anti-inflammatory; antiallergic; antitumor; antiproliferative;

KW osteopathic; dermatological; neuroprotective; virucide; antidiabetic;

KW cytoskeletal; anti-HIV; vasotropic; immunomodulator; neurological disease;

KW immune response disease; muscular disease; cancer;

KW modulating vesicular trafficking; tumour suppression;

KW signal transduction; protein sorting; membrane polarity; apoptosis;

KW synapse formation; multi-protein complex; leukocyte activation inhibitor.

XX Unidentified.

XX WO2003014303-A2.

XX 20-FEB-2003.

XX 02-AUG-2002; 2002WO-US024655.

XX 03-AUG-2001; 2001US-0309841P.

XX 25-FEB-2002; 2002US-0360061P.

XX (ARBO-) ARBOR VITA CORP.

PI Lu PS, Rabinowitz JD, Schweizer J, Carrick DM;  
 XX WPI; 2003-268193/26.  
 XX  
 PT PDZ ligand protein, is a peptide having few residues of C-terminal  
 PT sequence of PDZ ligand protein.  
 XX  
 XX Example 7, Page 152; 172pp; English.  
 XX  
 CC The invention relates to a novel modulator of binding between a PDZ  
 CC protein (post-synaptic density protein 95 (PSD95), Drosophila large disc  
 CC protein and Zonula Occludin 1 protein (ZO-1)) and a PDZ ligand (PL)  
 CC protein. The modulator is a peptide having 3 residues of a C-terminal  
 CC sequence of a PL protein. PDZ and PL proteins are a binding pair given in  
 CC specification, or a peptide mimetic of the 3 residue PL protein, or a  
 CC small molecule having similar functional activity as the 3 residue PL  
 CC protein. The reagents of the invention have the following activities:  
 CC antiinflammatory, antiallergic, antitumor, antidiabetic, osteopathic,  
 CC dermatological, neuroprotective, antiviral, antiparasitic, antiasthmatic,  
 CC antirheumatic, immunosuppressive, antithrombotic, cytostatic, anti-  
 CC HIV, vasotropic, and immunomodulator. The novel modulator is useful for  
 CC treating a disease correlated with binding between a PDZ protein and PL  
 CC protein. The disease can be a neurological disease, immune response  
 CC disease, muscular disease or cancer. The modulator is useful for  
 CC modulating vesicular trafficking, tumour suppression, signal  
 CC transduction, protein sorting, establishment of membrane polarity,  
 CC apoptosis, regulation of immune response and organisation of synapse  
 CC formation. The modulator is useful for facilitating the assembly of multi-  
 CC -protein complexes, often serving as a bridge between several proteins,  
 CC or regulating the function of other proteins, and to inhibit leukocyte  
 CC activation. The modulator is useful for treating diseases characterised  
 CC by inflammatory and humoral immune responses e.g., inflammation, allergy,  
 CC inflammatory bowel diseases, ulcerative colitis, psoriasis, asthma,  
 CC allergic rhinitis, atopic dermatitis, arthritis, multiple sclerosis,  
 CC diabetes, osteoarthritis, graft-versus-host diseases, atherosclerosis,  
 CC leukemias, infectious diseases (viral infection such as human  
 CC immunodeficiency virus (HIV)), and leukaemia. This sequence represents a  
 CC PDZ ligand (PL) protein of the invention.  
 XX  
 XX Sequence 103 AA;  
 SQ  
 Query Match 100.0%; Score 528; DB 7; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-60;  
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYVSV 60  
 DB 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYVSV 60  
 QY 61 NDTCVLGHTHAQQVKIFQSIPIGASVDELICRGYPLPFPDD 101  
 DB 61 NDTCVLGHTHAQQVKIFQSIPIGASVDELICRGYPLPFPDD 101  
 RESULT 4  
 ADIS3477  
 ID ADIS3477 standard; protein; 104 AA.  
 XX  
 XX ADIS3477;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human PDZ domain for GST fusion protein #120.  
 XX  
 KM Human; PDZ domain; postsynaptic density-disc-large-ZO-1; HPV infection;  
 KM E6 protein; cervical cancer; cytostatic.  
 OS Homo sapiens.  
 XX  
 XX US2004018487-A1.  
 PN  
 XX  
 PD 29-JAN-2004.

XX  
 PF 29-JUL-2003; 2003US-00630590.  
 XX  
 PR 10-NOV-2000; 2000US-00710059.  
 PR 16-FEB-2001; 2001US-0269523P.  
 PR 03-AUG-2001; 2001US-0309841P.  
 PR 19-FEB-2002; 2002US-0080273.  
 PR 25-FEB-2002; 2002US-0360061P.  
 PR 02-AUG-2002; 2002MO-US024655.  
 PR 09-SEP-2002; 2002US-0409298P.  
 PR 27-FEB-2003; 2003US-0450464P.  
 XX  
 PA (LUPS/) LU P. S.  
 PA (SCHW/) SCHWEIZER J.  
 PA (DIAZ/) DIAZ-SARMIENTO C. S.  
 PA (BELM/) BELMARES M. P.  
 PI Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;  
 DR WPI; 2004-122015/12.  
 XX  
 XX Detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 PT protein in a sample by contacting a sample suspected of containing an  
 PT oncogenic HPV E6 protein with a PDZ domain polypeptide.  
 XX  
 PS Disclosure; SEQ ID NO 120; 168pp; English.  
 XX  
 CC The invention relates to detecting the presence of an oncogenic human  
 CC papilloma virus (HPV) E6 protein in a sample comprising contacting the  
 CC sample with a PDZ domain polypeptide (postsynaptic density, disc-large,  
 CC ZO-1) and detecting any binding of the oncogenic HPV E6 protein in the  
 CC sample to the PDZ domain polypeptide. Also included are a system for  
 CC detecting the presence of an oncogenic HPV E6 polypeptide in a sample  
 CC (comprising a first and a second binding partner for an oncogenic HPV E6  
 CC polypeptide), where the first binding partner is a PDZ domain protein and  
 CC at least one of the binding partners is attached to a solid support, the  
 CC second binding partner being an anti-E6 antibody, determining if a  
 CC subject is infected with an oncogenic strain of HPV and a kit for testing  
 CC for the presence of oncogenic HPV E6 protein (the kit comprising first  
 CC and second binding partners for the oncogenic HPV E6 protein, where the  
 CC first binding partner is a PDZ domain protein). In the method of  
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 CC protein in a sample, the PDZ domain polypeptide comprises the amino acids  
 CC sequence of human Magi-1 PDZ domain 2. The PDZ domain peptide binds to  
 CC HPV E6 protein encoded by HPV strains 16, 18 and 45. The sample is  
 CC contacted with multiple PDZ domain polypeptides. The PDZ protein is a  
 CC fusion protein with GST (glutathione-S-transferase). The method is a  
 CC performed as part of a test for cervical cancer. The method is useful for  
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 CC protein in a sample thereby detecting HPV infection and possible risk of  
 CC cervical cancer. The present sequence is a human PDZ domain suitable for  
 CC inclusion in the test system of the invention.  
 XX  
 XX Sequence 104 AA;  
 SQ  
 Query Match 100.0%; Score 528; DB 8; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-60;  
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYVSV 60  
 DB 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYVSV 60  
 QY 61 NDTCVLGHTHAQQVKIFQSIPIGASVDELICRGYPLPFPDD 101  
 DB 61 NDTCVLGHTHAQQVKIFQSIPIGASVDELICRGYPLPFPDD 101  
 RESULT 5  
 ADM33568  
 ID ADM33568 standard; protein; 104 AA.  
 XX  
 XX ADM33568;  
 XX

XX 03-JUN-2004 (first entry)  
DT Human PDZ domain polypeptide #120.  
DE human papillomavirus; HPV; PDZ domain; HPV E6; cervical cancer;  
KW Magi-1 PDZ domain 2.  
XX Homo sapiens.  
OS  
PN WO2004022006-A2.  
PD 18-MAR-2004.  
XX  
XX 09-SEP-2003; 2003WO-US028508.  
PF  
XX 09-SEP-2002; 2002US-0409298P.  
PR 27-FEB-2003; 2003US-0450464P.  
PR 25-JUL-2003; 2003US-0490094P.  
PR 29-JUL-2003; 2003US-00630590.  
XX  
XX (ARBO-) ARBOR VITA CORP.  
XX  
XX Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;  
PI  
XX MPI; 2004-248368/23.  
XX  
XX Determining if a human subject is infected with an oncogenic strain of  
PT human papillomavirus (HPV) by detecting the presence of any oncogenic HPV  
PT E6 protein bound to the PDZ domain polypeptide using an HPV E6 binding  
PT partner.  
XX  
XX  
PS Disclosure; SEQ ID NO 120; 234pp; English.  
XX  
XX The invention relates to a method of determining if a human subject is  
CC infected with an oncogenic strain of human papillomavirus (HPV).  
CC Determining if a human subject is infected with an oncogenic strain of  
CC human papillomavirus (HPV) comprises: (1) contacting a sample obtained  
CC from the subject with a PDZ domain polypeptide bound to a solid support;  
CC and (2) detecting the presence of any oncogenic HPV E6 protein bound to  
CC the PDZ domain polypeptide using an HPV E6 binding partner, where the  
CC presence of oncogenic HPV E6 protein indicates that the subject is  
CC infected with an oncogenic strain of HPV. The method is performed in  
CC conjunction with histological analysis of the sample as part of a test  
CC for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ  
CC domain polypeptide binds to HPV E6 protein encoded by HPV strains 16, 18  
CC or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is  
CC directly or indirectly bound to the solid support. The PDZ binding  
CC partner is a labelled antibody that binds to the oncogenic HPV E6  
CC polypeptide. The sample is a cervical scrape, biopsy or lavage. The  
CC present sequence represents a PDZ domain polypeptide used in the method  
CC of the invention.  
XX  
XX  
SQ Sequence 104 AA;  
Query Match 100.0%; Score 528; DB 8; Length 104;  
Best Local Similarity 100.0%; Pred. No. 4.7e-60;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PSELKGFHTHTLKRSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60  
DB 1 PSELKGFHTHTLKRSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60  
QY 61 NPTCVLGHTHAQVVKIFOSIPIGASVDLELCRGYPLPPDP 101  
DB 61 NPTCVLGHTHAQVVKIFOSIPIGASVDLELCRGYPLPPDP 101  
RESULT 6  
ADO20999 standard; peptide; 104 AA.  
XX  
XX ADO20999;  
AC

XX 26-AUG-2004 (first entry)  
DT PDZ domain polypeptide #120.  
DE neuroprotective; gene therapy; N-methyl-D-aspartate receptor;  
KW NMDA receptor; PDZ domain; PDZ protein; binding inhibitor;  
KW neuronal disorder; stroke; ischemia; PDZ domain.  
XX  
XX Unidentified.  
OS  
PN WO2004045535-A2.  
PD 03-JUN-2004.  
XX  
XX 14-NOV-2003; 2003WO-US036698.  
PF  
XX 14-NOV-2002; 2002US-0426212P.  
PR 14-NOV-2002; 2002US-0426213P.  
XX  
XX (ARBO-) ARBOR VITA CORP.  
XX  
XX Lu PS, Garman JD, Belmares MP;  
PI  
XX MPI; 2004-420526/39.  
XX  
XX  
XX New pharmaceutical composition comprising a polypeptide that inhibits  
PT binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein,  
PT useful in treating a neuronal disorder e.g. an injury caused by stroke or  
PT ischemia.  
XX  
XX  
PS Example 9; Page 120; 146pp; English.  
XX  
XX The invention describes a pharmaceutical composition comprising an  
CC isolated, recombinant or synthetic polypeptide that inhibits binding  
CC between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a  
CC carrier, diluent or excipient and that comprises a C-terminal amino acid  
CC sequence of X-Thr-X-Val/Leu/Ala. Also described are: an isolated,  
CC recombinant or synthetic polypeptide for use in therapy and that  
CC comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and  
CC inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ  
CC protein; and a method for determining whether a test compound inhibits  
CC binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor.  
CC The pharmaceutical composition is useful in treating a neuronal disorder,  
CC which is an injury caused by stroke or ischemia. This is the amino acid  
CC sequence of a PDZ domain used to produce GST-PDZ fusion proteins.  
XX  
XX  
SQ Sequence 104 AA;  
Query Match 100.0%; Score 528; DB 8; Length 104;  
Best Local Similarity 100.0%; Pred. No. 4.7e-60;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PSELKGFHTHTLKRSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60  
DB 1 PSELKGFHTHTLKRSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60  
QY 61 NPTCVLGHTHAQVVKIFOSIPIGASVDLELCRGYPLPPDP 101  
DB 61 NPTCVLGHTHAQVVKIFOSIPIGASVDLELCRGYPLPPDP 101  
RESULT 7  
ADM33781 standard; protein; 108 AA.  
XX  
XX ADM33781;  
AC  
XX 03-JUN-2004 (first entry)  
DT Human PDZ domain/pGEX-3x #3.  
XX  
XX Human papillomavirus; HPV; PDZ domain; HPV E6; cervical cancer;  
KW

KM Magi-1 PDZ domain 2; human.  
XX Homo sapiens.  
OS Synthetic.  
XX WO2004022006-A2.  
XX 18-MAR-2004.  
XX 09-SEP-2003; 2003WO-US028508.  
XX 09-SEP-2002; 2002US-0409298P.  
XX 27-FEB-2003; 2003US-0450464P.  
XX 25-JUL-2003; 2003US-0490094P.  
XX 29-JUL-2003; 2003US-00630590.  
XX (ARBO-) ARBOR VITA CORP.  
XX Lu P8, Schweizer J, Diaz-Sarmiento CS, Belmares MP;  
XX WPI; 2004-248368/23.  
XX  
XX Determining if a human subject is infected with an oncogenic strain of  
XX human papillomavirus (HPV) by detecting the presence of any oncogenic HPV  
XX B6 protein bound to the PDZ domain polypeptide using an HPV B6 binding  
XX partner.  
XX  
XX Example 4; Page 97; 234pp; English.  
XX  
XX The invention relates to a method of determining if a human subject is  
XX infected with an oncogenic strain of human papillomavirus (HPV).  
XX Determining if a human subject is infected with an oncogenic strain of  
XX human papillomavirus (HPV) comprises: (1) contacting a sample obtained  
XX from the subject with a PDZ domain polypeptide bound to a solid support;  
XX and (2) detecting the presence of any oncogenic HPV B6 protein bound to  
XX the PDZ domain polypeptide using an HPV B6 binding partner, where the  
XX presence of oncogenic HPV B6 protein indicates that the subject is  
XX infected with an oncogenic strain of HPV. The method is performed in  
XX conjunction with histological analysis of the sample as part of a test  
XX for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ  
XX domain polypeptide binds to HPV B6 protein encoded by HPV strains 16, 18  
XX or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is  
XX directly or indirectly bound to the solid support. The PDZ binding  
XX partner is a labelled antibody that binds to the oncogenic HPV B6  
XX polypeptide. The sample is a cervical scrape, biopsy or lavage. The  
XX present sequence represents a human PDZ domain/pdEX-3X used in the method  
XX of the invention.  
XX  
XX Sequence 108 AA;  
XX  
XX  
XX Query Match 100.0%; Score 528; DB 8; Length 108;  
XX Best Local Similarity 100.0%; Pred. No. 5e-60;  
XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 PSELKGFHTTKRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIVSV 60  
XX 3 PSELKGFHTTKRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIVSV 62  
XX  
XX QY 61 NDTCVLGHTRAAQVVKIFQSIPIGASVDLRCRGVPLPFPDD 101  
XX 63 NDTCVLGHTRAAQVVKIFQSIPIGASVDLRCRGVPLPFPDD 103  
XX  
XX Db  
XX  
XX RESULT 8  
XX ABP63188  
XX ID ABP63188 standard; peptide; 263 AA.  
XX  
XX AC ABP63188;  
XX  
XX DT 28-OCT-2002 (first entry)  
XX  
XX DE Human WWP3 PDZ domain amino acid sequence.  
XX

KM Molecular interaction; haematopoietic cell; immune response; T cell;  
KM PDZ domain; B cell; endothelial cell; PDZ protein; PSD9; PDZ ligand;  
KM Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;  
KM immunosuppressive; antiinflammatory; antiallergic; antineuroleptic;  
KM anticancer; antiparasitic; dermatological; antiaesthetic; cytostatic;  
KM antimicrobial; vasotropic; inflammatory immune response; inflammation;  
KM humoral immune response; autoimmune disease; allergy; ulcerative colitis;  
KM inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;  
KM inflammatory dermatosis; respiratory allergic disease; asthma; cancer;  
KM allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;  
KM angiogenesis-dependent disorder; infectious disease.  
XX  
XX Homo sapiens.  
XX  
XX WO200242422-A2.  
XX  
XX 30-MAY-2002.  
XX  
XX 09-NOV-2001; 2001WO-US044138.  
XX  
XX 11-NOV-2000; 2000US-00710059.  
XX 24-NOV-2000; 2000US-00721915.  
XX 24-NOV-2000; 2000US-00722069.  
XX 28-NOV-2000; 2000US-00724553.  
XX  
XX (ARBO-) ARBOR VITA CORP.  
XX  
XX Lu P, Rabinowitz JD, Schweizer J;  
XX WPI; 2002-608221/65.  
XX  
XX Modulating the biological function of an endothelial cell or  
XX hemopoietic cell e.g., a T-cell or B-cell comprises introducing into  
XX the cell, an agent that inhibits binding of a PDZ protein and a PDZ  
XX ligand protein in the cell.  
XX  
XX Disclosure; Page 49-50; 207pp; English.  
XX  
XX The present invention describes a method (M1) for modulating a biological  
XX function of an endothelial cell or haematopoietic cell. M1 comprises  
XX introducing into the cell, an agent that inhibits binding of a PDZ  
XX (PSD9), Drosophila large disc protein, and Zonula Occludin 1 protein)  
XX protein and a PDZ ligand (PL) protein in the cell, and so modulates the  
XX biological function. Also described is a method (M2) for determining  
XX whether a test compound is an inhibitor of binding between a PDZ protein  
XX and a PL protein. M1 is used for modulating a biological function of an  
XX endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an  
XX inflammatory or humoral immune response, or an autoimmune disease. An  
XX inhibitor (I) is useful for treating a disease characterised by leukocyte  
XX activation, where the disease is characterised by an inflammatory or  
XX humoral immune response, e.g., an autoimmune disease. The compounds e.g.,  
XX PL-PDZ interaction inhibitors are useful for treating (ameliorating  
XX symptoms of) a variety of diseases and conditions characterised by  
XX inflammatory and humoral immune responses e.g., inflammation, allergy,  
XX inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,  
XX psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic  
XX diseases such as asthma, allergic rhinitis, transplantation rejection  
XX (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,  
XX autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,  
XX angiogenesis-dependent disorders, infectious diseases and ischaemia.  
XX AB096620 to AB096732 and ABP63153 to ABP63578 represent sequences used in  
XX the exemplification of the present invention  
XX  
XX Sequence 263 AA;  
XX  
XX  
XX Query Match 100.0%; Score 528; DB 5; Length 263;  
XX Best Local Similarity 100.0%; Pred. No. 1.7e-59;  
XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 PSELKGFHTTKRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIVSV 60  
XX 1 PSELKGFHTTKRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIVSV 60  
XX

QY 61 NDTICVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDP 101  
 ID 61 NDTICVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDP 101  
 Db

## RESULT 9

AD153658 standard; protein; 99 AA.  
 AD153658;  
 AD153658;  
 22-APR-2004 (first entry)  
 Human MAGI 1 PDZ domain 2 version 10.  
 Human; PDZ domain; postsynaptic density-large-ZO-1; HPV infection;  
 E6 protein; cervical cancer; cytosolic; MAGI 1.  
 Homo sapiens.  
 Synthetic.  
 US2004018487-A1.  
 29-JUN-2004.  
 29-JUL-2003; 2003US-00630590.  
 10-NOV-2000; 2000US-00710059.  
 16-FEB-2001; 2001US-0269523P.  
 03-AUG-2001; 2001US-0309841P.  
 19-FEB-2002; 2002US-00080273.  
 25-FEB-2002; 2002US-0360061P.  
 02-AUG-2002; 2002WO-US024655.  
 09-SEP-2002; 2002US-0409298P.  
 27-FEB-2003; 2003US-0450464P.  
 (LUPB/) LU P. S.  
 (SCHW/) SCHWEIZER J.  
 (DIAZ/) DIAZ-SARMIENTO C. S.  
 (BELM/) BELMARES M. P.

Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;  
 MPI; 2004-122015/12.

Detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 protein in a sample by contacting a sample suspected of containing an  
 oncogenic HPV E6 protein with a PDZ domain polypeptide.

Disclosure; SEQ ID NO 301; 168pp; English.

The invention relates to detecting the presence of an oncogenic human  
 papilloma virus (HPV) E6 protein in a sample comprising contacting the  
 sample with a PDZ domain polypeptide (postsynaptic density, disc-large,  
 ZO-1) and detecting any binding of the oncogenic HPV E6 protein in the  
 sample to the PDZ domain polypeptide. Also included are a system for  
 detecting the presence of an oncogenic HPV E6 polypeptide in a sample  
 comprising a first and a second binding partner for an oncogenic HPV E6  
 polypeptide, where the first binding partner is a PDZ domain protein and  
 at least one of the binding partners is attached to a solid support, the  
 second binding partner being an anti-E6 antibody), determining if a  
 subject is infected with an oncogenic strain of HPV and a kit for testing  
 for the presence of oncogenic HPV E6 protein (the kit comprising first  
 and second binding partners for the oncogenic HPV E6 protein, where the  
 first binding partner is a PDZ domain protein). In the method of  
 detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 protein in a sample, the PDZ domain polypeptide comprises the amino acids  
 sequence of human Magi-1 PDZ domain 2. The PDZ domain peptide binds to  
 HPV E6 protein encoded by HPV strains 16, 18 and 45. The sample is  
 contacted with multiple PDZ domain polypeptides. The PDZ protein is a  
 fusion protein with GST (glutathione-S-transferase). The method is a  
 performed as part of a test for cervical cancer. The method is useful for  
 detecting the presence of an oncogenic human papilloma virus (HPV) E6

CC protein in a sample thereby detecting HPV infection and possible risk of  
 CC cervical cancer. The present sequence is a PDZ domain from human MAGI 1  
 CC which may be modified. Note:AD153650-AD153687 are listed in the sequence  
 CC listing and named in table 9, but are not further described in the  
 CC specification.  
 CC

SO Sequence 99 AA;

Query Match 97.5%; Score 515; DB 8; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 2,1e-58;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEIKGKFHTKLRKSSRGFGFTVVGDEPDEFLOIKSLVLDGPALDGMETGDTVSVN 61  
 DB 1 SEIKGKFHTKLRKSSRGFGFTVVGDEPDEFLOIKSLVLDGPALDGMETGDTVSVN 60

QY 62 DTICVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDP 100  
 DB 61 DTICVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDP 99

## RESULT 10

ADM33749  
 ID ADM33749 standard; protein; 99 AA.  
 ADM33749;  
 ADM33749;  
 03-JUN-2004 (first entry)  
 Human MAGI-1 PDZ domain 2 #9.  
 Human MAGI-1 PDZ domain 2; human.  
 human papillomavirus; HPV; PDZ domain; HPV E6; cervical cancer;  
 Magi-1 PDZ domain 2; human.  
 Homo sapiens.

WO2004022006-A2.  
 18-MAR-2004.  
 09-SEP-2003; 2003WO-US028508.  
 09-SEP-2002; 2002US-0409298P.  
 27-FEB-2003; 2003US-0450464P.  
 25-JUL-2003; 2003US-0490094P.  
 29-JUL-2003; 2003US-00630590.  
 (ARBO-) ARBOR VITA CORP.

Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;  
 MPI; 2004-248368/23.

Determining if a human subject is infected with an oncogenic strain of  
 human papillomavirus (HPV) by detecting the presence of any oncogenic HPV  
 E6 protein bound to the PDZ domain polypeptide using an HPV E6 binding  
 partner.

Example 15; SEQ ID NO 301; 234pp; English.

The invention relates to a method of determining if a human subject is  
 infected with an oncogenic strain of human papillomavirus (HPV).  
 Determining if a human subject is infected with an oncogenic strain of  
 human papillomavirus (HPV) comprises: (1) contacting a sample obtained  
 from the subject with a PDZ domain polypeptide bound to a solid support;  
 and (2) detecting the presence of any oncogenic HPV E6 protein bound to  
 the PDZ domain polypeptide using an HPV E6 binding partner, where the  
 presence of oncogenic HPV E6 protein indicates that the subject is  
 infected with an oncogenic strain of HPV. The method is performed in  
 conjunction with histological analysis of the sample as part of a test  
 for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ  
 domain polypeptide binds to HPV E6 protein encoded by HPV strains 16, 18  
 or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is

CC directly or indirectly bound to the solid support. The PDZ binding  
 CC partner is a labelled antibody that binds to the oncogenic HPV E6  
 CC polypeptide. The sample is a cervical scrape, biopsy or lavage. The  
 CC present sequence represents a human Magi-1 PDZ domain 2 used in the  
 CC method of the invention.

SO Sequence 99 AA;

Query Match 97.5%; Score 515; DB 8; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-58;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEIKGKFIHTKLRKSRGFGFTVVGSDPEDEFLQIKSLVLDGPAALDGKMETGDIIVSVN 61  
 DB 1 SEIKGKFIHTKLRKSRGFGFTVVGSDPEDEFLQIKSLVLDGPAALDGKMETGDIIVSVN 60  
 QY 62 DTCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDD 100  
 DB 61 DTCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDD 99

RESULT 11

AAU87919 standard; protein; 740 AA.

AAU87919;

05-JUN-2002 (first entry)

Human PDZP2 protein.

Human: PDZ domain; MW domain; rat; cow; mouse; fruitfly; protein therapy;  
 KM gene therapy; PDZ-mediated disease; inward potassium channel; WBP;  
 KM dimer inhibitor peptide; carboxylate binding loop.

Homo sapiens.

MO200207751-A1.

31-JAN-2002.

24-JUL-2001; 2001MO-US023269.

25-JUL-2000; 2000US-0221215P.

28-NOV-2000; 2000US-00723810.

(AXCE-) AXCELL BIOSCIENCES CORP.

Herrero J, Pirozzi G, Uveges A;

WPI; 2002-195842/25.

N-PSDB; ABK46531.

Methods for identifying polypeptides comprising PDZ domains, the  
 PT polypeptides and their encoding nucleic acids, useful for the diagnosis  
 PT and treatment of PDZ related disorders.

Claim 43; Fig 10; 225pp; English.

The invention relates to methods for identifying polypeptides comprising  
 CC PDZ domains, and their encoding nucleic acids. The sequences are used to  
 CC identify modulators of their expression, function and activity, for use  
 CC in the diagnosis and treatment of PDZ related disorders. Antibodies  
 CC against the proteins and cells that produce them may be used for the  
 CC treatment of PDZ-mediated disease states. Sequences AAU87943-AAU87974  
 CC represent proteins containing PDZ domains, fragments of these proteins  
 CC and other related peptides used in the methods of the invention

Sequence 740 AA;

Query Match 97.3%; Score 514; DB 5; Length 740;  
 Best Local Similarity 98.0%; Pred. No. 4.4e-57;  
 Matches 99; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PSEIKGKFIHTKLRKSRGFGFTVVGSDPEDEFLQIKSLVLDGPAALDGKMETGDIIVSV 60

DB 128 PSEIKGKFIHTKLRKSRGFGFTVVGSDPEDEFLQIKSLVLDGPAALDGKMETGDIIVSV 187

QY 61 NDTCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDD 101

DB 188 NDTCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDD 228

Query Match 97.5%; Score 515; DB 8; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-58;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AD153657 standard; protein; 94 AA.

AD153657;

22-APR-2004 (first entry)

Human MAGI 1 PDZ domain 2 version 9.

Human: PDZ domain; postsynaptic density-large-ZO-1; HPV infection;  
 KM E6 protein; cervical cancer; cytosolic; MAGI 1.

Homo sapiens.

Synthetic.

US2004018487-A1.

29-JAN-2004.

29-JUL-2003; 2003US-00630590.

10-NOV-2000; 2000US-00710059.

16-FEB-2001; 2001US-0269523P.

03-AUG-2001; 2001US-0309841P.

19-FEB-2002; 2002US-0080273P.

25-FEB-2002; 2002US-0360061P.

02-AUG-2002; 2002MO-US024655.

09-SEP-2002; 2002US-0409298P.

27-FEB-2003; 2003US-0450464P.

(LUPS/) LU P S.

(SCHW/) SCHWEITZER J.

(DIAZ/) DIAZ-SARMIENTO C S.

(BELM/) BELMARES M P.

Lu PS, Schweitzer J, Diaz-Sarmiento CS, Belmares MP;

WPI; 2004-122015/12.

Detecting the presence of an oncogenic human papilloma virus (HPV) E6

protein in a sample by contacting a sample suspected of containing an

oncogenic HPV E6 protein with a PDZ domain polypeptide.

Disclosure; SEQ ID NO 300; 168pp; English.

The invention relates to detecting the presence of an oncogenic human  
 CC papilloma virus (HPV) E6 protein in a sample comprising contacting the  
 CC sample with a PDZ domain polypeptide (postsynaptic density, disc-large,  
 CC ZO-1) and detecting any binding of the oncogenic HPV E6 protein in the  
 CC sample to the PDZ domain polypeptide. Also included are a system for  
 CC detecting the presence of an oncogenic HPV E6 polypeptide in a sample  
 CC (comprising a first and a second binding partner for an oncogenic HPV E6  
 CC polypeptide, where the first binding partner is a PDZ domain protein and  
 CC at least one of the binding partners is attached to a solid support, the  
 CC second binding partner being an anti-E6 antibody), determining if a  
 CC subject is infected with an oncogenic strain of HPV and a kit for testing  
 CC for the presence of oncogenic HPV E6 protein (the kit comprising first  
 CC and second binding partners for the oncogenic HPV E6 protein, where the  
 CC first binding partner is a PDZ domain protein). In the method of  
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 CC protein in a sample, the PDZ domain polypeptide comprises the amino acids  
 CC sequence of human Magi-1 PDZ domain 2. The PDZ domain peptide binds to

CC HPV E6 protein encoded by HPV strains 16, 18 and 45. The sample is  
 CC contacted with multiple PDZ domain polypeptides. The PDZ protein is a  
 CC fusion protein with GST (glutathione-S-transferase). The method is a  
 CC performed as part of a test for cervical cancer. The method is useful for  
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 CC protein in a sample thereby detecting HPV infection and possible risk of  
 CC cervical cancer. The present sequence is a PDZ domain from human MAGI 1  
 CC which may be modified. Note: AD153650-AD153687 are listed in the sequence  
 CC listing and named in table 9, but are not further described in the  
 CC specification.

XX SQ Sequence 94 AA;

Query Match 91.9%; Score 485; DB 8; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-54;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DQ 3 ELKGRFHTKLRKSRGFGFTVVGDEPDEFLQISLVLDGPALDGMETGDIYSVND 62  
 1 ELKGRFHTKLRKSRGFGFTVVGDEPDEFLQISLVLDGPALDGMETGDIYSVND 60

DQ 63 TCVLGHHTAQQVVKIFQSIPIGASVDLELCRGYPL 96  
 61 TCVLGHHTAQQVVKIFQSIPIGASVDLELCRGYPL 94

#### RESULT 13

ID ADM33748 standard; protein; 94 AA.

AC ADM33748;

DT 03-JUN-2004 (first entry)

DE Human Magi-1 PDZ domain 2 #8.

KM human papillomavirus; HPV; PDZ domain; HPV E6; cervical cancer;

KW Magi-1 PDZ domain 2; human.

OS Homo sapiens.

PN MO2004022006-A2.

PD 18-MAR-2004.

PF 09-SEP-2003; 2003WC-US028508.

PR 09-SEP-2002; 2002US-0409298P.

PR 27-FEB-2003; 2003US-0450464P.

PR 25-JUL-2003; 2003US-0490094P.

PR 29-JUL-2003; 2003US-00630590.

PA (ARBO-) ARBOR VITA CORP.

PI Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;

DR WPI; 2004-248368/23.

PT Determining if a human subject is infected with an oncogenic strain of

PT human papillomavirus (HPV) by detecting the presence of any oncogenic HPV

PT E6 protein bound to the PDZ domain polypeptide using an HPV E6 binding

PT partner.

PI Example 15; SEQ ID NO 300; 234pp; English.

XX The invention relates to a method of determining if a human subject is  
 CC infected with an oncogenic strain of human papillomavirus (HPV).  
 CC Determining if a human subject is infected with an oncogenic strain of  
 CC human papillomavirus (HPV) comprises: (1) contacting a sample obtained  
 CC from the subject with a PDZ domain polypeptide bound to a solid support;  
 CC and (2) detecting the presence of any oncogenic HPV E6 protein bound to  
 CC the PDZ domain polypeptide using an HPV E6 binding partner, where the  
 CC presence of oncogenic HPV E6 protein indicates that the subject is

CC infected with an oncogenic strain of HPV. The method is performed in  
 CC conjunction with histological analysis of the sample as part of a test  
 CC for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ  
 CC domain polypeptide binds to HPV E6 protein encoded by HPV strains 16, 18  
 CC or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is  
 CC directly or indirectly bound to the solid support. The PDZ binding  
 CC partner is a labelled antibody that binds to the oncogenic HPV E6  
 CC polypeptide. The sample is a cervical scrape, biopsy or lavage. The  
 CC present sequence represents a human Magi-1 PDZ domain 2 used in the  
 CC method of the invention.

XX SQ Sequence 94 AA;

Query Match 91.9%; Score 485; DB 8; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-54;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DQ 3 ELKGRFHTKLRKSRGFGFTVVGDEPDEFLQISLVLDGPALDGMETGDIYSVND 62  
 1 ELKGRFHTKLRKSRGFGFTVVGDEPDEFLQISLVLDGPALDGMETGDIYSVND 60

DQ 63 TCVLGHHTAQQVVKIFQSIPIGASVDLELCRGYPL 96  
 61 TCVLGHHTAQQVVKIFQSIPIGASVDLELCRGYPL 94

#### RESULT 14

ID AD153654 standard; protein; 88 AA.

AC AD153654;

DT 22-APR-2004 (first entry)

DE Human MAGI 1 PDZ domain 2 version 6.

KM Human; PDZ domain; postnaptic density-large-ZO-1; HPV infection;

KW E6 protein; cervical cancer; cytostatic; MAGI 1.

OS Homo sapiens.

PN US2004018487-A1.

PD 29-JAN-2004.

PF 29-JUL-2003; 2003US-00630590.

PR 10-NOV-2000; 2000US-00710059.

PR 16-FEB-2001; 2001US-0269523P.

PR 03-AUG-2001; 2001US-0309841P.

PR 19-FEB-2002; 2002US-00080273.

PR 25-FEB-2002; 2002US-0360061P.

PR 02-AUG-2002; 2002WC-US024655.

PR 09-SEP-2002; 2002US-0409298P.

PR 27-FEB-2003; 2003US-0450464P.

PA (LUPS/) Lu P S.

PA (SCHW/) SCHWEIZER J.

PA (DIAZ/) DIAZ-SARMIENTO C S.

PA (BELM/) BELMARES M P.

PI Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;

DR WPI; 2004-122015/12.

PT Detecting the presence of an oncogenic human papilloma virus (HPV) E6

PT protein in a sample by contacting a sample suspected of containing an

PT oncogenic HPV E6 protein with a PDZ domain polypeptide.

PI Disclosure; SEQ ID NO 297; 168pp; English.

XX The invention relates to detecting the presence of an oncogenic human



CC papilloma virus (HPV) E6 protein in a sample comprising contacting the  
 CC sample with a PDZ domain polypeptide (postsynaptic density, disc-large,  
 CC ZO-1) and detecting any binding of the oncogenic HPV E6 protein in the  
 CC sample to the PDZ domain polypeptide. Also included are a system for  
 CC detecting the presence of an oncogenic HPV E6 polypeptide in a sample  
 CC (comprising a first and a second binding partner for an oncogenic HPV E6  
 CC polypeptide, where the first binding partner is a PDZ domain protein and  
 CC at least one of the binding partners is attached to a solid support, the  
 CC second binding partner being an anti-E6 antibody), determining if a  
 CC subject is infected with an oncogenic strain of HPV and a kit for testing  
 CC for the presence of oncogenic HPV E6 protein (the kit comprising first  
 CC and second binding partners for the oncogenic HPV E6 protein, where the  
 CC first binding partner is a PDZ domain protein). In the method of  
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 CC protein in a sample, the PDZ domain polypeptide comprises the amino acids  
 CC sequence of human Magi-1 PDZ domain 2. The PDZ domain peptide binds to  
 CC HPV E6 protein encoded by HPV strains 16, 18 and 45. The sample is  
 CC contacted with multiple PDZ domain polypeptides. The PDZ protein is a  
 CC fusion protein with GST (glutathione-S-transferase). The method is a  
 CC performed as part of a test for cervical cancer. The method is useful for  
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6  
 CC protein in a sample thereby detecting HPV infection and possible risk of  
 CC cervical cancer. The present sequence is a PDZ domain from human MAGI 1  
 CC which may be modified. Note: AD153650-AD153687 are listed in the sequence  
 CC listing and named in table 9, but are not further described in the  
 CC specification.

XX Seq Sequence 88 AA;

Query Match Best Local Similarity 100.0%; Pred. No. 8,1e-51; Length 88;

Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FHTKLKSSRGFGFTVGGDEPDEPLQIKSLVLDGPALDGMKMTGDIIVSVNDTCVLG 67  
 1 FHTKLKSSRGFGFTVGGDEPDEPLQIKSLVLDGPALDGMKMTGDIIVSVNDTCVLG 60

DB 68 HTHAQVVKIFOSIPIGASVDELRCRGP 95  
 61 HTHAQVVKIFOSIPIGASVDELRCRGP 88

RESULT 15

ID ADM33745 standard; protein; 88 AA.

XX AC ADM33745;

XX DT 03-JUN-2004 (first entry)

XX DE Human Magi-1 PDZ domain 2 #5.

XX KM human papillomavirus; HPV; PDZ domain; HPV E6; cervical cancer;

XX KM Magi-1 PDZ domain 2; human.

XX OS Homo sapiens.

XX PN WO2004022006-A2.

XX PD 18-MAR-2004.

XX PF 09-SEP-2003; 2003MO-US028508.

XX PR 09-SEP-2002; 2002JUS-0409298P.

XX PR 27-FEB-2003; 2003JUS-0450046P.

XX PR 25-JUL-2003; 2003JUS-0490094P.

XX PR 29-JUL-2003; 2003JUS-00630590.

XX PA (ARBO-) ARBOR VITA CORP.

XX PI Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;

XX WPI; 2004-248366/23.

XX PT Determining if a human subject is infected with an oncogenic strain of  
 PT human papillomavirus (HPV) by detecting the presence of any oncogenic HPV  
 PT E6 protein bound to the PDZ domain polypeptide using an HPV E6 binding  
 PT partner.

XX PS Example 15; SEQ ID NO 297; 234pp; English.

XX The invention relates to a method of determining if a human subject is  
 CC infected with an oncogenic strain of human papillomavirus (HPV).  
 CC Determining if a human subject is infected with an oncogenic strain of  
 CC human papillomavirus (HPV) comprises: (1) contacting a sample obtained  
 CC from the subject with a PDZ domain polypeptide bound to a solid support;  
 CC and (2) detecting the presence of any oncogenic HPV E6 protein bound to  
 CC the PDZ domain polypeptide using an HPV E6 binding partner, where the  
 CC presence of oncogenic HPV E6 protein indicates that the subject is  
 CC infected with an oncogenic strain of HPV. The method is performed in  
 CC conjunction with histological analysis of the sample as part of a test  
 CC for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ  
 CC domain polypeptide binds to HPV E6 protein encoded by HPV strains 16, 18  
 CC or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is  
 CC directly or indirectly bound to the solid support. The PDZ binding  
 CC partner is a labelled antibody that binds to the oncogenic HPV E6  
 CC polypeptide. The sample is a cervical scrape, biopsy or lavage. The  
 CC present sequence represents a human Magi-1 PDZ domain 2 used in the  
 CC method of the invention.

XX Seq Sequence 88 AA;

Query Match Best Local Similarity 100.0%; Pred. No. 8,1e-51; Length 88;

Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FHTKLKSSRGFGFTVGGDEPDEPLQIKSLVLDGPALDGMKMTGDIIVSVNDTCVLG 67  
 1 FHTKLKSSRGFGFTVGGDEPDEPLQIKSLVLDGPALDGMKMTGDIIVSVNDTCVLG 60

DB 68 HTHAQVVKIFOSIPIGASVDELRCRGP 95  
 61 HTHAQVVKIFOSIPIGASVDELRCRGP 88

Search completed: December 20, 2004, 14:18:59  
 Job time : 155 secs





STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,804  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/596,291  
FILING DATE: 09-AUG-1996  
APPLICATION NUMBER: US 08/115,573  
FILING DATE: 01-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09943  
FILING DATE: 01-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: L0461/7003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
TELEX:  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-09-100-804-23

Query Match 22.1%; Score 116.5; DB 3; Length 79;  
Best Local Similarity 40.0%; Pred. No. 7.8e-08;  
Matches 26; Conservative 10; Mismatches 24; Indels 5; Gaps 2;

QY 15 KSSRGFTVVG-DEP---DEFLQIKSLVLDGPALDGMETGDIYVSVNDTCVLGH 69  
DB 1 KNSGJGFSTAGSTIDNPHIGTSTIYTKLISGAAADGRISINDIVSVNDVAVDP 60

QY 70 HAQV 74  
DB 61 HAQAV 65

RESULT 3  
US-09-290-640-46  
Sequence 46, Application US/09290640  
Patent No. 6204055  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Marcuseon, Eric G.  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-0351  
CURRENT APPLICATION NUMBER: US/09/290,640  
FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 46  
LENGTH: 2485  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-290-640-46

Query Match 22.0%; Score 116; DB 3; Length 2485;  
Best Local Similarity 35.6%; Pred. No. 1.1e-05;  
Matches 26; Conservative 18; Mismatches 25; Indels 4; Gaps 2;

QY 13 LKSSR-GFTVVGDEP---DEFLQIKSLVLDGPALDGMETGDIYVSVNDTCVLGH 68  
DB 1096 LKDKATYGLGFQIGKKGRIDLGIFFISSVAPGADLDGCLKPDRLISVSVLEGV 1155

QY 69 THAQVKIFOSIP 81  
DB 1156 SHHAIEILQNP 1168

RESULT 4  
US-09-665-615B-46  
Sequence 46, Application US/09665615B  
Patent No. 6653133  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Marcuseon, Eric G.  
TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-0502  
CURRENT APPLICATION NUMBER: US/09/665,615B  
FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/290,640  
FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 179  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 46  
LENGTH: 2485  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-665-615B-46

Query Match 22.0%; Score 116; DB 4; Length 2485;  
Best Local Similarity 35.6%; Pred. No. 1.1e-05;  
Matches 26; Conservative 18; Mismatches 25; Indels 4; Gaps 2;

QY 13 LKSSR-GFTVVGDEP---DEFLQIKSLVLDGPALDGMETGDIYVSVNDTCVLGH 68  
DB 1096 LKDKATYGLGFQIGKKGRIDLGIFFISSVAPGADLDGCLKPDRLISVSVLEGV 1155

QY 69 THAQVKIFOSIP 81  
DB 1156 SHHAIEILQNP 1168

RESULT 5  
US-09-306-998-3  
Sequence 3, Application US/09306998  
Patent No. 6291173  
GENERAL INFORMATION:  
APPLICANT: Bartel, Paul L.  
APPLICANT: Tavligian, Sean V.  
TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein  
FILE REFERENCE: MMSC2  
CURRENT APPLICATION NUMBER: US/09/306,998  
FILING DATE: 1999-05-07  
EARLIER APPLICATION NUMBER: US 60/084,740  
FILING DATE: 1998-05-08  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 2037  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-306-998-3

Query Match 21.1%; Score 111.5; DB 3; Length 2037;  
Best Local Similarity 30.2%; Pred. No. 3.4e-05;  
Matches 29; Conservative 22; Mismatches 38; Indels 7; Gaps 3;

```

Patent No. 60664472
GENERAL INFORMATION:
APPLICANT: GOMEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLASSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P. C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: LC461/7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-100-804-3

Query Match 20.9%; Score 110.5; DB 3; Length 2465;
Best Local Similarity 34.7%; Pred. No. 6e-05;
Matches 25; Conservative 17; Mismatches 27; Indels 3; Gaps 2;

QY 13 LRKSR-GFGFTVGGD--EPDELQIKSLVLDGPALDGMETGDIIVSYNDVCVIGT 69
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1077 LKDKARKGLGQIRIGGKMETDIDRIFSSVAPGSPADPFHGCLKGRDLISVNSVLEGS 1136
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 70 HAQVVKFQSIIP 81
|:::|:::|
Db 1137 HMAAIEILQNP 1148

RESULT 8
US-09-562-737-51
Sequence 51, Application US/09562737
Patent No. 6428867
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UMSW0708
CURRENT APPLICATION NUMBER: US/09/562,737

```

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CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 51
LENGTH: 206
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-51

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Query Match	20.7%	Score 109.5	DB 4	Length 206
Best Local Similarity	30.1%	Pred. No. 2.5e-06		
Matches 28	Conservative 17	Mismatches 41	Indels 7	Gaps 2

```

QY      13 LRKSRGFGFTVVGDEP-----DEFLQIKSLVLDGPAALDQKMETGVIYVINDTCVLG 67
      | : ||| : | : : | | | | | : | | | | :
Db      77 LTRGSGGLGNIWGTDDQQYVNSDGGIYVSRIKEDGAARDRLQEGPKILSYNGQDLKN 136

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QY      68 HTHAQVVKLFQSIPIGASVDLELCRGYPLEFDP 100
          |  |  |  |  |  |  |  |  |  |  |  |  |
Db      137 LTHQDAVDLEFRN--AGYAVSLRWQHRKLPVQNGP 167

```

```

RESULT 9
US-09-513-999C-7700
; Sequence 7700, Application US/0951399C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7700
; LENGTH: 99
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-513-999C-7700

```

Query Match	20.2%	Score 106.5	DB 4	Length 99
Best Local Similarity	31.3%	Pred. No. 2.3e-06		
Matches	26	Conservative 17	Mismatches 33	Indels 7
Gaps	2			

  

Oy	13	LKRSRGGFVTVGGDEP----	DEFLDIKSLVLDGPPALDQKMEGTGYIVSVNDPTVLG	67
Db	16	LTRGSGGLGFENIVGSTDQOYVNSDSGITVYSRIKENGAAALDGRLOEGDKILSVNGDILKN		75
Oy	68	HTHAQVVKIFOSIPIGASVDLEL	90	
Db	76	LHODAVDLFRN--AGYAVSLRV	96	

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RESULT 10
US-09-270-767-3346
; Sequence 33346, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 33346
;
; LENGTH: 204
;
; TYPE: PRT
;
; ORGANISM: Drosophila melanogaster
US-09-270-767-33346

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Query Match	20.1%	Score 106	DB 4	length 204
Best Local Similarity	32.8%	Pred. No. 7.4e-06		
Matches 22	Conservative 15	Mismatches 30	Indels 0	Gaps 0

09  
12 KLRSSRRGFTVVGGDEDFLLKSLVDGPALDGRKETGAVIVSVNDTCVLGHHTA 71  
104 ELPTTBEGIGFNWVGKKEQNSPIYISRIIPGCVADRHGGLKRGDQLLSVNGSVSEBENH 163

QY	72 QVVKIFQ 78
	: :::
Db	164 KAVELLK 170

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RESULT 11
US-09-270-767-48563
; Sequence 48563, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48563
; LENGTH: 204
; TYPE: prt
; ORGANISM: Drosophila melanogaster
US-09-270-767-48563

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Query March	20.1%	Score 106;	DB 4;	Length 204;
Best Local Similarity	32.8%;	Pred. No. 7.4e-06;		
Matches	22;	Conservative 15;	Mismatches 30;	Indels 0; Gaps 0
OY	12	KLRKSRGFGPTVVGDEPDEFLOIKSLVTLGPALDQKMETGDIVAVNDTCVLGHTRHA	71	
	:::::	:::::	:::::	:::::
Dd	104	ELPTEBGLGNWGGKEQNSPFIYSRIIPGVADRHGGLRKGDQLLSVNGSVGEENHE	163	
OY	72	QVVKIFQ	78	
	:::::	:::::		
Dd	164	KAVELLK	170	

```

RESULT 12
US-09-151-611-1
: Sequence 1, Application US/09151611
: Patent No. 5958731
: GENERAL INFORMATION:
: APPLICANT: Yue, Henry
: APPLICANT: Au-Young, Janice
: APPLICANT: Patterson, Chandra
: TITLE OF INVENTION: CELF JUCTION PDZ PROTEIN
: FILE REFERENCE: PE-0599 US
: CURRENT FILING DATE: 1998-09-11
: CURRENT APPLICATION NUMBER: US/09/151,611
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: PERL Program
: SEQ ID NO 1
: LENGTH: 233
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:-
: OTHER INFORMATION: 1974337
US-09-151-611-1

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Query Match	20.1%;	Score 106;	DB 2;	Length 233;
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Best Local Similarity 32.4%; Pred. No. 8.9e-06;  
Matches 22; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 12 KLRKSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIVSVNDTCVLGHTHA 71

DB 110 ELPTDEGLGFNVWGKESQSPYISRIIPGVAEHRRGGLKRGDQLSVNGSVSGEHHH 169

QY 72 QVVKIFOS 79

DB 170 KAVELLKA 177

## RESULT 13

US-09-370-102-1

Sequence 1, Application US/09370102

Patent No. 6255547

GENERAL INFORMATION:

APPLICANT: Yue, Henry

APPLICANT: Au-Young, Janice

APPLICANT: Patterson, Chandra

TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN

FILE REFERENCE: PF-0599 US

CURRENT APPLICATION NUMBER: US/09/370,102

CURRENT FILING DATE: 1999-08-06

EARLIER APPLICATION NUMBER: 09/151,611

EARLIER FILING DATE: 1998-09-11

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PERL Program

SEQ ID NO 1

LENGTH: 233

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: -

OTHER INFORMATION: 1974337

US-09-370-102-1

Query Match

Best Local Similarity 32.4%; Score 106; DB 3; Length 233;

Matches 22; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 12 KLRKSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIVSVNDTCVLGHTHA 71

DB 110 ELPTDEGLGFNVWGKESQSPYISRIIPGVAEHRRGGLKRGDQLSVNGSVSGEHHH 169

QY 72 QVVKIFOS 79

DB 170 KAVELLKA 177

## RESULT 14

US-09-080-855-12

Sequence 12, Application US/09080855A

Patent No. 6083721

GENERAL INFORMATION:

APPLICANT: Saras, Jan

APPLICANT: Franz, Petra

APPLICANT: Aspenstrm, Pontus

APPLICANT: Hellman, Ulf

APPLICANT: Genez, Leonel Jorge

TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1

FILE REFERENCE: 10461/7030

CURRENT APPLICATION NUMBER: US/09/080,855A

CURRENT FILING DATE: 1998-05-18

EARLIER APPLICATION NUMBER: 08/805,583

EARLIER FILING DATE: 1997-02-25

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 2466

TYPE: PRT

ORGANISM: Homo sapiens

US-09-080-855-12

Query Match 19.3%; Score 105; DB 3; Length 2466;

Best Local Similarity 32.9%; Pred. No. 0.00033;

Matches 24; Conservative 18; Mismatches 27; Indels 4; Gaps 2;

QY 13 LKRSR-GFGFTVVGDEP---DEFLQIKSLVLDGPALDGMETGDIVSVNDTCVLGH 68

DB 1077 LKDKAKYGLGFQITIGSKMGRDLGIFISSVAPGADPFHGCCKPGDRLISVNSVLEGV 1136

QY 69 THAQVVKIFOSIP 81

DB 1137 SHRAAIEILLQAP 1149

## RESULT 15

US-09-566-076-12

Sequence 12, Application US/09566076

Patent No. 6475775

GENERAL INFORMATION:

APPLICANT: Saras, Jan

APPLICANT: Franz, Petra

APPLICANT: Aspenstrm, Pontus

APPLICANT: Hellman, Ulf

APPLICANT: Genez, Leonel Jorge

APPLICANT: Heidlin, Carl-Henrik

TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1

FILE REFERENCE: 10461/7030

CURRENT APPLICATION NUMBER: US/09/566,076

CURRENT FILING DATE: 1998-05-18

EARLIER APPLICATION NUMBER: 09/080,855

EARLIER FILING DATE: 1998-05-18

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 2466

TYPE: PRT

ORGANISM: Homo sapiens

US-09-566-076-12

Query Match

Best Local Similarity 32.9%; Score 105; DB 4; Length 2466;

Matches 24; Conservative 18; Mismatches 27; Indels 4; Gaps 2;

QY 13 LKRSR-GFGFTVVGDEP---DEFLQIKSLVLDGPALDGMETGDIVSVNDTCVLGH 68

DB 1077 LKDKAKYGLGFQITIGSKMGRDLGIFISSVAPGADPFHGCCKPGDRLISVNSVLEGV 1136

QY 69 THAQVVKIFOSIP 81

DB 1137 SHRAAIEILLQAP 1149

Search completed: December 20, 2004, 14:23:47

Job time : 42 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 14:22:26 ; Search time 146 Seconds  
(without alignments)  
247.543 Million cell updates/sec

Title: US-10-630-590-288

Perfect score: 528

Sequence: 1 PSLKCKPHTTKRKSSRGF.....IGASVDLELCRGYPLPPDP 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubppa/PCR\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep:\*
- 4: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata/1/pubppa/PCRUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/prodata/1/pubppa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/prodata/1/pubppa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/prodata/1/pubppa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/prodata/1/pubppa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 18: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	528	100.0	101	US-10-630-590-288	Sequence 288, App
2	528	100.0	101	US-10-789-102-70	Sequence 70, App
3	528	100.0	104	US-10-630-590-120	Sequence 120, App
4	528	100.0	104	US-10-789-102-219	Sequence 219, App
5	515	97.5	99	US-10-630-590-301	Sequence 301, App
6	515	97.5	99	US-10-789-102-328	Sequence 328, App
7	485	91.9	94	US-10-630-590-300	Sequence 300, App
8	485	91.9	94	US-10-789-102-327	Sequence 327, App
9	456	86.4	88	US-10-630-590-297	Sequence 297, App
10	456	86.4	88	US-10-789-102-324	Sequence 324, App
11	452	85.6	88	US-10-630-590-298	Sequence 298, App
12	452	85.6	88	US-10-789-102-325	Sequence 325, App
13	436	82.6	85	US-10-630-590-295	Sequence 295, App

14	436	82.6	85	17	US-10-789-102-322	Sequence 322, App
15	415	78.6	81	15	US-10-630-590-299	Sequence 299, App
16	415	78.6	81	17	US-10-789-102-326	Sequence 326, App
17	399	75.6	78	15	US-10-630-590-296	Sequence 296, App
18	399	75.6	78	17	US-10-789-102-323	Sequence 323, App
19	391	74.1	76	15	US-10-630-590-294	Sequence 294, App
20	391	74.1	76	17	US-10-789-102-321	Sequence 321, App
21	386	73.1	104	15	US-10-630-590-9	Sequence 9, App1
22	386	73.1	104	17	US-10-789-102-108	Sequence 108, App
23	367	69.5	72	15	US-10-630-590-293	Sequence 293, App
24	367	69.5	72	17	US-10-789-102-320	Sequence 320, App
25	365	69.1	72	15	US-10-630-590-304	Sequence 304, App
26	365	69.1	72	15	US-10-630-590-311	Sequence 311, App
27	365	69.1	72	17	US-10-789-102-331	Sequence 331, App
28	365	69.1	72	17	US-10-789-102-338	Sequence 338, App
29	364	68.9	72	15	US-10-630-590-302	Sequence 302, App
30	364	68.9	72	15	US-10-630-590-305	Sequence 305, App
31	364	68.9	72	15	US-10-630-590-306	Sequence 306, App
32	364	68.9	72	15	US-10-630-590-307	Sequence 307, App
33	364	68.9	72	15	US-10-630-590-309	Sequence 309, App
34	364	68.9	72	15	US-10-630-590-310	Sequence 310, App
35	364	68.9	72	15	US-10-630-590-312	Sequence 312, App
36	364	68.9	72	15	US-10-630-590-313	Sequence 313, App
37	364	68.9	72	15	US-10-630-590-321	Sequence 321, App
38	364	68.9	72	17	US-10-789-102-329	Sequence 329, App
39	364	68.9	72	17	US-10-789-102-332	Sequence 332, App
40	364	68.9	72	17	US-10-789-102-333	Sequence 333, App
41	364	68.9	72	17	US-10-789-102-334	Sequence 334, App
42	364	68.9	72	17	US-10-789-102-336	Sequence 336, App
43	364	68.9	72	17	US-10-789-102-337	Sequence 337, App
44	364	68.9	72	17	US-10-789-102-339	Sequence 339, App
45	364	68.9	72	17	US-10-789-102-340	Sequence 340, App

#### ALIGNMENTS

RESULT 1  
US-10-630-590-288  
; Sequence 288, Application US/10630590  
; Publication No. US20040018487A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter  
; APPLICANT: Schweitzer, Johannes  
; APPLICANT: Diaz-Sarmiento, Chomorrow Samoza  
; APPLICANT: Belmonte, Michael P.  
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER  
; FILE REFERENCE: VITA-008  
; CURRENT APPLICATION NUMBER: US/10/630,590  
; CURRENT FILING DATE: 2003-07-29  
; PRIOR APPLICATION NUMBER: 60/409,298  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/450,464  
; PRIOR FILING DATE: 2003-02-27  
; PRIOR APPLICATION NUMBER: US 02/24655  
; PRIOR FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 10/080,273  
; PRIOR FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 60/269,523  
; PRIOR FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: 09/710,059  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 330  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 288  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-630-590-288

```
Query Match      100.0%; Score 528; DB 15; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
DB      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
QY      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101
      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101
DB      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101
      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101

RESULT 2
US-10-789-102-70
; Sequence 70; Application US/10789102
; Publication No. US20040229298A1
; GENERAL INFORMATION:
; APPLICANT: LU, Peter S
; APPLICANT: BAGOWSKI, Christoph Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: Garman, Jonathan David
; APPLICANT: BELMARES, MICHAEL P
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; FILE REFERENCE: VITA-009
; CURRENT APPLICATION NUMBER: US/10/789,102
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-102-70

Query Match      100.0%; Score 528; DB 17; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
DB      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
QY      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101
      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101
DB      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101
      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101

RESULT 3
US-10-630-590-120
; Sequence 120; Application US/10630590
; Publication No. US20040018487A1
```

```
; GENERAL INFORMATION:
; APPLICANT: LU, Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-590-120

Query Match      100.0%; Score 528; DB 15; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.5e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
DB      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
      1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
QY      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101
      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101
DB      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101
      61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPDPD 101

RESULT 4
US-10-789-102-219
; Sequence 219; Application US/10789102
; Publication No. US20040229298A1
; GENERAL INFORMATION:
; APPLICANT: LU, Peter S
; APPLICANT: BAGOWSKI, Christoph Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: Garman, Jonathan David
; APPLICANT: BELMARES, MICHAEL P
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; FILE REFERENCE: VITA-009
; CURRENT APPLICATION NUMBER: US/10/789,102
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
```

```

; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-102-219
```

```

Query Match          100.0%; Score 528; DB 17; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.5e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 PSELKGFHTKLRKSSRGFGFTVVGDEPDEFLQISLVLDGPAALDGKMETGDIYVSV 60
    |||||
Db 1 PSELKGFHTKLRKSSRGFGFTVVGDEPDEFLQISLVLDGPAALDGKMETGDIYVSV 60
    |||||

QY 61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGVPLPDPD 101
    |||||
Db 61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGVPLPDPD 101
    |||||
```

```

RESULT 5
US-10-630-590-301
; Sequence 301, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Samoza
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 301
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-590-301
```

```

Query Match          97.5%; Score 515; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-55;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 SELKGFHTKLRKSSRGFGFTVVGDEPDEFLQISLVLDGPAALDGKMETGDIYVSV 61
    |||||
Db 1 SELKGFHTKLRKSSRGFGFTVVGDEPDEFLQISLVLDGPAALDGKMETGDIYVSV 60
    |||||
```

```

QY 62 DTCVLGHHTAQQVKIFQSIPIGASVDLELCRGVPLPDPD 100
    |||||
Db 61 DTCVLGHHTAQQVKIFQSIPIGASVDLELCRGVPLPDPD 99
    |||||
```

```

RESULT 6
US-10-789-102-328
; Sequence 328, Application US/10789102
; Publication No. US20040229298A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S
; APPLICANT: BAGOWSKI, Christoph Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: Gattam, Jonathan David
; APPLICANT: BELMARES, MICHAEL P
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; FILE REFERENCE: VITA-009
; CURRENT APPLICATION NUMBER: US/10/789,102
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-102-328
```

```

Query Match          97.5%; Score 515; DB 17; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-55;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 SELKGFHTKLRKSSRGFGFTVVGDEPDEFLQISLVLDGPAALDGKMETGDIYVSV 61
    |||||
Db 1 SELKGFHTKLRKSSRGFGFTVVGDEPDEFLQISLVLDGPAALDGKMETGDIYVSV 60
    |||||

QY 62 DTCVLGHHTAQQVKIFQSIPIGASVDLELCRGVPLPDPD 100
    |||||
Db 61 DTCVLGHHTAQQVKIFQSIPIGASVDLELCRGVPLPDPD 99
    |||||
```

```

RESULT 7
US-10-630-590-300
; Sequence 300, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Samoza
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; CURRENT FILING DATE: 2003-07-29
```

```

; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-590-300

```

```

Query Match          91.9%; Score 485; DB 15; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.5e-51;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 ELKGKFIHTKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVND 62
        |||||||
DB      1 ELKGKFIHTKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVND 60
        |||||||
QY      63 TCVLGHTHAQVVKIFOSIPIGASVDLELCRGYP 96
        |||||||
DB      61 TCVLGHTHAQVVKIFOSIPIGASVDLELCRGYP 94
        |||||||

```

```

RESULT 8
US-10-789-102-327
; Sequence 327, Application US/10789102
; Publication No. US20040229298A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S
; APPLICANT: BAGOWSKI, Christoph Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: Garmen, Jonathan David
; APPLICANT: BELMARES, MICHAEL P
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; FILE REFERENCE: VITA-009
; CURRENT APPLICATION NUMBER: US/10/789,102
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 327
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-102-327

```

```

Query Match          91.9%; Score 485; DB 17; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.5e-51;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 ELKGKFIHTKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVND 62
        |||||||
DB      1 ELKGKFIHTKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVND 60
        |||||||
QY      63 TCVLGHTHAQVVKIFOSIPIGASVDLELCRGYP 96
        |||||||
DB      61 TCVLGHTHAQVVKIFOSIPIGASVDLELCRGYP 94
        |||||||

```

```

RESULT 9
US-10-630-590-297
; Sequence 297, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Somoza
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-590-297

```

```

Query Match          86.4%; Score 456; DB 15; Length 88;
Best Local Similarity 100.0%; Pred. No. 8.2e-48;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 FIHTKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVLG 67
        |||||||
DB      1 FIHTKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVLG 60
        |||||||
QY      68 HTHAQVVKIFOSIPIGASVDLELCRGYP 95
        |||||||
DB      61 HTHAQVVKIFOSIPIGASVDLELCRGYP 88
        |||||||

```

```

RESULT 10
US-10-789-102-324
; Sequence 324, Application US/10789102
; Publication No. US20040229298A1

```

```
/ GENERAL INFORMATION:
/ APPLICANT: LU, Peter S
/ APPLICANT: BAGOWSKI, Christoph Peter
/ APPLICANT: SCHWEIZER, Johannes
/ APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
/ APPLICANT: Garman, Jonathan David
/ APPLICANT: BELMARES, MICHAEL P
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: CERVICAL CANCER
/ FILE REFERENCE: VITA-009
/ CURRENT APPLICATION NUMBER: US/10/789,102
/ CURRENT FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: 10/630,590
/ PRIOR FILING DATE: 2003-07-29
/ PRIOR APPLICATION NUMBER: 60/490,094
/ PRIOR FILING DATE: 2003-07-25
/ PRIOR APPLICATION NUMBER: 60/450,464
/ PRIOR FILING DATE: 2003-02-27
/ PRIOR APPLICATION NUMBER: US02/24655
/ PRIOR FILING DATE: 2002-08-02
/ PRIOR APPLICATION NUMBER: 60/309,841
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: 60/360,061
/ PRIOR FILING DATE: 2002-02-25
/ PRIOR APPLICATION NUMBER: 10/080,273
/ PRIOR FILING DATE: 2002-02-19
/ PRIOR APPLICATION NUMBER: 60/269,523
/ PRIOR FILING DATE: 2002-02-16
/ PRIOR APPLICATION NUMBER: 09/710,059
/ PRIOR FILING DATE: 2000-11-10
/ NUMBER OF SEQ ID NOS: 357
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 324
/ LENGTH: 88
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-789-102-324

Query Match      86.4%; Score 456; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 8.2e-48;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FHHTKLRKSRGFGFTVGGDEPDEFLQIKSLVLDGPAALDGKMETGDIIVSVNDTCVLG 67
DB      1 FHHTKLRKSRGFGFTVGGDEPDEFLQIKSLVLDGPAALDGKMETGDIIVSVNDTCVLG 60

QY      68 HTHAQQVKIFQSIPIGASVDLELCRGYP 95
DB      61 HTHAQQVKIFQSIPIGASVDLELCRGYP 88

RESULT 11
US-10-630-590-298
/ Sequence 298, Application US/10630590
/ Publication No. US20040018487A1
/ GENERAL INFORMATION:
/ APPLICANT: LU, Peter
/ APPLICANT: SCHWEIZER, Johannes
/ APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
/ APPLICANT: Belmares, Michael P.
/ TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
/ FILE REFERENCE: VITA-008
/ CURRENT APPLICATION NUMBER: US/10/630,590
/ CURRENT FILING DATE: 2003-07-29
/ PRIOR APPLICATION NUMBER: 60/409,298
/ PRIOR FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: 60/450,464
/ PRIOR FILING DATE: 2003-02-27
/ PRIOR APPLICATION NUMBER: US 02/24655
/ PRIOR FILING DATE: 2002-08-02
/ PRIOR APPLICATION NUMBER: 60/309,841
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: 60/360,061
```

```
/ PRIOR FILING DATE: 2002-02-25
/ PRIOR APPLICATION NUMBER: 10/080,273
/ PRIOR FILING DATE: 2002-02-19
/ PRIOR APPLICATION NUMBER: 60/269,523
/ PRIOR FILING DATE: 2001-02-16
/ PRIOR APPLICATION NUMBER: 09/710,059
/ PRIOR FILING DATE: 2000-11-10
/ NUMBER OF SEQ ID NOS: 330
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 298
/ LENGTH: 88
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-630-590-298

Query Match      85.6%; Score 452; DB 15; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.5e-47;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KGKFIHTKLRKSRGFGFTVGGDEPDEFLQIKSLVLDGPAALDGKMETGDIIVSVNDTC 64
DB      1 KGKFIHTKLRKSRGFGFTVGGDEPDEFLQIKSLVLDGPAALDGKMETGDIIVSVNDTC 60

QY      65 VLGHTHAQQVKIFQSIPIGASVDLELCR 92
DB      61 VLGHTHAQQVKIFQSIPIGASVDLELCR 88

RESULT 12
US-10-789-102-325
/ Sequence 325, Application US/10789102
/ Publication No. US20040229298A1
/ GENERAL INFORMATION:
/ APPLICANT: LU, Peter S
/ APPLICANT: BAGOWSKI, Christoph Peter
/ APPLICANT: SCHWEIZER, Johannes
/ APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
/ APPLICANT: Garman, Jonathan David
/ APPLICANT: BELMARES, MICHAEL P
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: CERVICAL CANCER
/ FILE REFERENCE: VITA-009
/ CURRENT APPLICATION NUMBER: US/10/789,102
/ CURRENT FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: 10/630,590
/ PRIOR FILING DATE: 2003-07-29
/ PRIOR APPLICATION NUMBER: 60/490,094
/ PRIOR FILING DATE: 2003-07-25
/ PRIOR APPLICATION NUMBER: 60/450,464
/ PRIOR FILING DATE: 2003-02-27
/ PRIOR APPLICATION NUMBER: US02/24655
/ PRIOR FILING DATE: 2002-08-02
/ PRIOR APPLICATION NUMBER: 60/309,841
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: 60/360,061
/ PRIOR FILING DATE: 2002-02-25
/ PRIOR APPLICATION NUMBER: 10/080,273
/ PRIOR FILING DATE: 2002-02-19
/ PRIOR APPLICATION NUMBER: 60/269,523
/ PRIOR FILING DATE: 2002-02-16
/ PRIOR APPLICATION NUMBER: 09/710,059
/ PRIOR FILING DATE: 2000-11-10
/ NUMBER OF SEQ ID NOS: 357
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 325
/ LENGTH: 88
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-789-102-325

Query Match      85.6%; Score 452; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.5e-47;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 KKKFHTKLKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTC 64
      |||
      1 KKKFHTKLKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTC 60
      |||

Db      65 VLGHTHAQVVKIFQSIPIGASVDLELCR 92
      |||
      61 VLGHTHAQVVKIFQSIPIGASVDLELCR 88
      |||

RESULT 13
US-10-630-590-295
; Sequence 295, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Samoza
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 85
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-630-590-295

Query Match      82.6%; Score 436; DB 15; Length 85;
Best Local Similarity 100.0%; Pred. No. 2,2e-45;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FHTHTKLKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVIG 67
      |||
      1 FHTHTKLKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVIG 60
      |||

Db      68 HTHAQVVKIFQSIPIGASVDLELCR 92
      |||
      61 HTHAQVVKIFQSIPIGASVDLELCR 85
      |||

RESULT 14
US-10-789-102-322
; Sequence 322, Application US/10789102
; Publication No. US20040229298A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S
; APPLICANT: BAGOWSKI, Christoph Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: GARMAN, Jonathan David
; APPLICANT: BELMARES, MICHAEL P
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; CERVICAL CANCER
```

```
; FILE REFERENCE: VITA-009
; CURRENT APPLICATION NUMBER: US/10/789,102
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 322
; LENGTH: 85
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-789-102-322

Query Match      82.6%; Score 436; DB 17; Length 85;
Best Local Similarity 100.0%; Pred. No. 2,2e-45;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FHTHTKLKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVIG 67
      |||
      1 FHTHTKLKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVIG 60
      |||

Db      68 HTHAQVVKIFQSIPIGASVDLELCR 92
      |||
      61 HTHAQVVKIFQSIPIGASVDLELCR 85
      |||

RESULT 15
US-10-630-590-299
; Sequence 299, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Samoza
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
```

SEQ ID NO 299  
LENGTH: 81  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-630-590-299

Query Match 78.6%; Score 415; DB 15; Length 81;  
Best Local Similarity 100.0%; Pred. No. 7.7e-43;  
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	5	KGKFIHTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPAALDGKMETGDIIVSVNDTC	64
DB	1	KGKFIHTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPAALDGKMETGDIIVSVNDTC	60
QY	65	VLGHTHAQVVKIFOSIPIGAS	85
DB	61	VLGHTHAQVVKIFOSIPIGAS	81

Search completed: December 20, 2004, 14:34:48  
Job time : 147 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 14:13:02; Search time 38 Seconds

(without alignments)  
255.734 Million cell updates/sec

Title: US-10-630-590-288

Perfect score: 528  
Sequence: 1 PSELKGRFHTKLRKSSRGF.....IGASVDLELCRGYPLEPDD 101

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR 79: \*  
2: PIR: \*  
3: PIR: \*  
4: PIR: \*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528	100.0	1171	T42372	probable guanylate
2	528	100.0	1256	JE0209	brain-specific ang
3	418	79.2	1277	T14152	synaptic scaffold
4	242.5	45.9	1012	T23160	hypothetical prote
5	127.5	24.1	1464	T13716	hazooka gene prote
6	121.5	23.0	960	A39651	disca-large tumor
7	121.5	23.0	1337	T13948	atypical protein k
8	116	22.0	2294	T167630	protein-tyrosine-p
9	116	22.0	2466	T167629	protein-tyrosine-p
10	116	22.0	2490	A54971	protein-tyrosine-p
11	115.5	21.9	852	T10811	channel associated
12	115.5	21.9	870	G01974	channel associated
13	114	21.6	2450	S71625	protein-tyrosine-p
14	112.5	21.3	904	T138757	homolog of Drosoph
15	112.5	21.3	926	T138756	homolog of Drosoph
16	110.5	20.9	2054	T46612	multi PDZ domain p
17	110.5	20.9	2055	T30259	multiple PDZ domai
18	109.5	20.7	269	T25079	hypothetical prote
19	109.5	20.7	293	D89193	protein T21C9.1 (1
20	109.5	20.7	2172	T20145	hypothetical prote
21	107.5	20.4	1131	T15617	hypothetical prote
22	106.5	20.2	911	T15652	tyrosine-associated
23	105	19.9	1112	T32733	AMPA glutamate rec
24	104.5	19.8	720	A45436	synapse-associated
25	104.5	19.8	724	UH0800	postsynaptic densi
26	104.5	19.8	767	T09599	postsynaptic densi
27	103	19.5	1944	A59438	KIAA1424 protein (
28	102	19.3	431	T16191	hypothetical prote
29	99	18.8	317	T27179	hypothetical prote

30	98	18.6	628	2	T09458	numb-binding prote
31	98	18.6	728	2	T09457	numb-binding prote
32	97.5	18.5	1666	2	T43169	hypothetical prote
33	96.5	18.3	357	2	S72575	hypothetical prote
34	96.5	18.3	1893	2	A56158	eye development pr
35	93.5	17.7	87	2	S60315	PSD-95-related pro
36	92.5	17.5	117	2	I81209	tyrosine phosphata
37	92.5	17.5	126	2	I81210	tyrosine phosphata
38	92.5	17.5	415	2	UC7167	C kinase 1 interac
39	92.5	17.5	416	2	A56486	perinuclear bindin
40	89	16.9	444	2	T15775	hypothetical prote
41	89	16.9	761	2	T15776	hypothetical prote
42	88	16.7	623	2	A49840	segment polarity p
43	86	16.3	817	2	T03852	protein phosphatase
44	85.5	16.2	352	2	T22159	hypothetical prote
45	85.5	16.2	1252	2	T14272	coractin-binding

#### ALIGNMENTS

##### RESULT 1

T42372 probable guanylate kinase (EC 2.7.4.8) 1, membrane-associated, splice form b - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T42372

R: Dobrosotckaya, I.; Guy, R.K.; James, G.L.

J. Biol. Chem. 272, 31589-31597, 1997

A:Title: MAGI-1, a membrane-associated guanylate kinase with a unique arrangement of pr

A:Reference number: Z22139; PMID:98058950; PMID:9395497

A:Accession: T42372

A:Status: preliminary; translated from GB/EMBL/DDB

A:Molecule type: mRNA

A:Residues: 1-1171 <DOB>

A:Cross-references: UNIPROT:O54893; EMBL:AF027503; NID:g2702346; PID:g2702347; PIDN:AAB

A:Experimental source: strain C57 Black/6 x CBA

C:Genetics:

A:Gene: Magi-1

C:Keywords: alternative splicing; phosphotransferase

F:300-337/Domain: WW repeat homology <MWR1>

F:347-384/Domain: WW repeat homology <MWR2>

Query Match 100.0%; Score 528; DB 2; Length 1171;

Best Local Similarity 100.0%; Pred. No. 3.9e-47;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGRFHTKLRKSSRGFTVVGDDPEFLQIKSLVLDGPAALDGMETGDIYSV 60

Db 443 PSELKGRFHTKLRKSSRGFTVVGDDPEFLQIKSLVLDGPAALDGMETGDIYSV 502

QY 61 NDTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLEPDD 101

Db 503 NDTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLEPDD 543

##### RESULT 2

JE0209

brain-specific angiogenesis inhibitor-associated protein 1 - human

N:Alternative names: BAII-associated protein 1; BAPI (mismomer)

C:Species: Homo sapiens (man)

C>Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 09-Jul-2004

C:Accession: JE0209

R: Shiratsuchi, T.; Futamura, M.; Oda, K.; Nishimori, H.; Nakamura, Y.; Tokino, T.

Biochem. Biophys. Res. Commun. 247, 597-604, 1998

A:Title: Cloning and characterization of BAI-associated protein 1: A PDZ domain-contain

A:Reference number: JE0209; PMID:98321173; PMID:9647739

A:Accession: JE0209

A:Molecule type: mRNA

A:Residues: 1-1256 <SHI>

A:Cross-references: UNIPROT:O75085; UNIPROT:Q96C27; GB:AB010894; NID:g3370997

A:Experimental source: brain

C:Genetics:

A:Gene: GDB:BAIAP1; BAP1  
 A:Cross-references: GDB:9864783  
 A:Map position: 3p14.1-3p14.1  
 F:300-337/Domain: WW repeat homology <WM1>  
 F:359-396/Domain: WW repeat homology <WM2>

Query Match 100.0%; Score 528; DB 2; Length 1256;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-47;  
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIIVSV 60  
 DB 463 PSELKGFHTTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIIVSV 522

QY 61 NDTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 101  
 DB 523 NDTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 563

#### RESULT 3

T14152

Synaptic scaffolding protein S-SCAM - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 15-Mar-2004

C:Accession: T14152

R:Hitrac, K.; Hata, Y.; Ide, N.; Takeuchi, M.; Irie, M.; Yao, I.; Deguchi, M.; Toyoda, A.

J. Biol. Chem. 273, 21105-21110, 1998

A:Title: A novel multiple PDZ domain-containing molecule interacting with N-methyl-D-aspartate

A:Reference number: Z17889; MUID:98361985; PMID:9694864

A:Accession: T14152

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1277 <HIR>

A:Cross-references: EMBL:AF034863; NID:G3411052; PID:G3411053; PIDN:AA031124.1

C:Genetics:

A:Gene: S-SCAM

C:Function:

A:Description: may assemble receptors and cell adhesion proteins at synaptic junctions

F:302-339/Domain: WW repeat homology <WM1>

F:348-385/Domain: WW repeat homology <WM2>

Query Match 79.2%; Score 418; DB 2; Length 1277;  
 Best Local Similarity 74.0%; Pred. No. 1.5e-35;  
 Matches 74; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 2 SELKGFHTTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIIVSV 61  
 DB 418 SELKGFHTTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIIVSV 477

QY 62 DTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 101  
 DB 478 DTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 517

RESULT 4  
 T23160  
 Hypothetical protein K01A6.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T23160

R:Courtesy: A.

submitted to the EMBL Data Library, January 1996

A:Reference number: Z19701

A:Accession: T23160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1012 <WII>

A:Cross-references: UNIPROT:Q21075; EMBL:Z68750; PIDN:CAA92965.1; GSPDB:GN00022; CESP:K0

A:Experimental source: clone K01A6

C:Genetics:

A:Gene: CESP:K01A6.1

A:Map position: 4

A:Introns: 107/1; 151/2; 183/2; 270/2; 316/3; 410/3; 628/3; 922/3; 971/3

F:131-168/Domain: WW repeat homology <WMR>

Query Match 45.9%; Score 242.5; DB 2; Length 1012;  
 Best Local Similarity 42.7%; Pred. No. 3e-17;  
 Matches 44; Conservative 25; Mismatches 31; Indels 3; Gaps 1;

QY 1 PSELKGFHTTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIIVSV 57  
 DB 373 PSELKGFHTTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIIVSV 432

QY 58 VSNVDTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 100  
 DB 433 VSNVDTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 475

#### RESULT 5

T13716

bazooka gene protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004

C:Accession: T13716

R:Kuchinke, U.; Grawe, F.; Knust, E.

submitted to the EMBL Data Library, November 1998

A:Description: Control of spindle orientation in Drosophila by the Par-3-related PDZ-dom

A:Reference number: Z17708

A:Accession: T13716

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1464 <KUC>

A:Cross-references: UNIPROT:O96782; EMBL:AJ130871; NID:e1363519; PID:e1363520; PIDN:CA01

C:Genetics:

A:Gene: bazooka

A:Cross-references: FlyBase:FBgn0000163

A:Map position: X

Query Match 24.1%; Score 127.5; DB 2; Length 1464;  
 Best Local Similarity 32.3%; Pred. No. 5.5e-05;  
 Matches 32; Conservative 19; Mismatches 45; Indels 3; Gaps 1;

QY 6 GKFTTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIIVSVND 62  
 DB 440 GKFTTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIIVSVND 499

QY 63 TCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 101  
 DB 500 TCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 538

RESULT 6  
 A39651  
 discs-large tumor suppressor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: A39651

R:Woods, D.F.; Bryant, P.J.

Cell 66, 451-464, 1991

A:Title: The discs-large tumor suppressor gene of Drosophila encodes a guanylate kinase

A:Reference number: A39651; MUID:91330294; PMID:1651165

A:Accession: A39651

A:Molecule type: mRNA

A:Residues: 1-960 <WOO>

A:Cross-references: UNIPROT:P31007; GB:M73529; NID:G157243; PIDN:AAA28468.1; PID:G157244

C:Comment: Loss of this protein causes large imaginal discs by allowing neoplastic overg

C:Keywords: signal transduction

F:45-123/Domain: G1GF domain homology <GLG1>

F:159-241/Domain: G1GF domain homology <GLG2>

F:491-563/Domain: G1GF domain homology <GLG3>

F:607-665/Domain: SH3 homology <SH3>

F;771-948/Domain: guanylate kinase homology <GKI>

Query Match	23.0%	Score 121.5	DB 1	Length 960
Best Local Similarity	39.7%	Pred. No. 0.00014		
Matches 27, Conservative	11	Mismatches 25	Indels 5	Gaps 2

```

QY      12  KLRSSRRGGFTVVG-DEP-----DEFLQKSLVLDGPALLDGKMETGADVIVNVDTCL 66
DB      42  QLEGGNSGGFGFSLGTDNPHIGTDSITYTKLLSGGAALDGRISINDIIVSVNVDSVV 101

```

```

QY      67 GHTHAQVV 74
          |||
Db      102 DVPHASAV 109

```

RESULT 7  
T13948

A:Typical protein kinase C isotype-specific interacting protein ASIP - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: J13948  
R:Zimmler, Y.; Hirose, T.; Tamai, Y.; Hirai, S.; Nagashima, Y.; Fujimoto, T.; Tabuse, Y.;  
J. Cell Biol. 143, 95-106, 1998  
A:Title: An atypical PKC directly associates and colocalizes at the epithelial tight junction  
A:Reference number: 217827; PMID:98437350; PMID:9765423  
A:Accession: J13948  
A:Status: Preliminary; translated from GB/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-1337 <ICU>  
A:Cross-references: UNIPROT:Q9Z340; EMBL:AB005549; NID:g3868777; PIDN:BAA34216.1; PID:g34216.1  
C:Genetic(s):  
/Gene: asbp

Query Match	23.0%;	Score 121.5;	DB 2;	Length 1337;
Similarity	28.0%;	Pred. No. 0.00021;		
Beet Local	26;	Conservative 32;	Indels 9;	Gaps 2;

QY 6 GKFIHTKLKKSSRGFGFTV-----VGGDPEDFEQIKSLVLDDGPAALDGMKMGCDVIYS 59  
Db 457 GKRLNIQLKKGTGGEGFSITSRDVTYIGSAP---IVYKNILPRGAIIDGRLLKGDRLLE 513

QY 60 VNDTCVLGHTHAQVVKIFOSIPICASVDLELCR 92  
|| : || : || : || : || :  
Db 514 VNGVDLAGKSOEEVSLIRSTKMEGTIVSLVER 546

RESULT 8  
167630  
Protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3 -  
C|Species: Homo sapiens (man)  
C|Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C|Accession: 167630  
R|Makawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.  
FEBS Lett. 337, 200-206, 1994  
A|Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane  
A|Reference number: 153483; MUID:94116679; PMID:8287977  
A|Accession: 167630  
A|Status: preliminary; translated from GB/EMBL/DBJ  
A|Molecule type: mRNA  
A|Residues: 1-2294 <RES>  
A|Cross-references: UNIPROT:Q12923; GB:D12111; NID:G452193; PIDN:BAA04752.1; PID:G452194  
C|Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13, GLGF domain homology;  
C|Keywords: phosphoric monoester hydrolase  
F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>  
F:1182-1258/Domain: GLGF domain homology <GLG2>  
F:2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>

```

Query Match      22.0%; Score 116; DB 2; Length 2294;
Best Local Similarity 35.6%; Pred. No. 0.0015;
Matches 26; Conservative 18; Mismatches 25; Indels 4; Gaps

QY 13 LRKSR-GFGTGVGDPE--DEFLQIKSLVLDGPALDQKKEIETGVISVNDTCVLGH 68
|:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Db 905 LKDAKYGLGFQIIGGEKMGRLLDGI FISSVAPGGPADLDGCLKPGDRLLISVNSVSLEGV 964

QY 69 THAQVKIFQSI P 81  
: : : : :  
Db 965 SHHAIETLQNA P 977

RESULT 9  
167629

C:Protein: tyrosine-phosphatase (EC 3.1.3.48)ppn13, nonreceptor type 13, splice form 2  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
 C:Accession: I67629  
 R:Magawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.  
 F:EBBS Lett. 337, 200-206, 1994  
 A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane  
 A:Reference number: 153483; MUID:9411679; PMID:8287977  
 A:Accession: I67629  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2466 <RES>  
 A:Cross-references: UNIPROT:O12923; GB:D1210; NID:9452191; PIDN:BAA04751.1; PID:945219  
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13, GSGF domain homology;  
 C:Keywords: phosphoric monoester hydrolase  
 F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:1354-1430/Domain: GSGF domain homology <G42>  
 F:12218-1437/Domain: protein-tyrosine-phosphatase homology <PTR>  
 F:12218-1437/Domain: protein-tyrosine-phosphatase homology <PTR>

Query Match	22.0%	Score 116;	DB 2;	Length 2466;
Best Local Similarity	35.6%	Pred. No. 0.0016;		
Matches 26;	Conservative 18;	Mismatches 25;	Indels 4;	Gaps 2;

QY 13 LKRSR-GFGFTVVGDEP---DEFLQIKSLVLDGDPALDGMKMETGDVIVSVNDTCVLGH 68

Db 1077 LKDDATYGEIGFOIIGGKMGRLDGIPISSVABGPPALDGCILKPGDILISVSVLSREV 1136

OY 69 THAQVVKRIPQSIIP 81  
:|::||:|  
Db 1137 SHHAAIEIQNAIP 1149

RESULT 10  
A54971  
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 1 [

N:Alternate names: Fas-associated phosphatase FAP-1; protein-tyrosine-phosphatase hPTP  
C:Species: Homo sapiens (man)  
C:Date: 11-Nov-1994 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
A:Accession: A54971, A55114, I59595, I53483, S46955  
R:Barville, D., Ahmad, S., Stocco, R., Shen, S.H.  
J. Biol. Chem. 269, 22320-22327, 1994  
A:Title: A novel protein-tyrosine phosphatase with homology to both the cytoskeletal pr  
A:Reference number: A54971, MUID:94350988, PMID:8071359  
A:Accession: A54971  
A:Molecule type: mRNA  
A:Residues: 1-2490 <BAN>  
A:Cross-references: UNIPROT:Q12923; GB:U12128  
A:Note: sequence shown follows authors' translation at positions 62-63  
R:Saras, J., Claesson-Welsh, L., Heldin, C.H., Gonor, L.J.  
J. Biol. Chem. 269, 24082-24089, 1994  
A:Title: Cloning and characterization of PTP11, a protein tyrosine phosphatase with sim  
A:Reference number: A55114, MUID:95014139, PMID:7929060  
A:Accession: A55114  
A:Molecule type: mRNA  
A:Residues: 1-61 'GS', 64-839, 'D', 841-1055, 1075-1133, 'FH', 1136-1210, 'I', 1212-1363, 1389-1  
A:Cross-references: GB:X00289, NID:G515030, PIDN:CA556563.1, PID:G515031  
R:Sato, T., Irie, S., Kitada, S., Reed, J.C.

A:Title: FAP-1: a protein tyrosine phosphatase that associates with Fas.  
 A:Reference number: 159595; MUID:95232528; PMID:753343  
 A:Accession: 159595  
 A:Status: translated from GR/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1279-1888 <RES>

A/Cross-references: GB:L34583; NID:g806291; PIDN:AAC41755.1; PID:g806292  
 R:Meekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.  
 FEBS Lett. 337, 200-206, 1994  
 A/Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane  
 A/Reference number: 153483; MUID:94116679; PMID:8287977  
 A/Accession: 153483  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-61, 'GS', 64-839, 'D', 841-1210, 'I', 1212-1383, 1389-2299, 'OM', 2302-2490 <RE2>  
 A/Cross-references: GB:D21209; NID:g452189; PIDN:BA04750.1; PID:g452190  
 C/Genetics: 8  
 A/Gene: GDB:PTPN13  
 A/Cross-references: GDB:306348; OMIM:600267  
 A/Map position: 4q21.3-q21.3  
 C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;  
 C/Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi  
 F:574-668/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:1099-1175/Domain: GLGF domain homology <GLG1>  
 F:1373-1454/Domain: GLGF domain homology <GLG2>  
 F:1511-1590/Domain: GLGF domain homology <GLG3>  
 F:1799-1870/Domain: GLGF domain homology <GLG4>  
 F:1893-1967/Domain: GLGF domain homology <GLG5>  
 F:2242-2461/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:2413/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:2419/Binding site: substrate phosphate (Arg) #status predicted

Query Match 22.0%; Score 116; DB 1; Length 2490;  
 Best Local Similarity 35.6%; Pred. No. 0.0016;  
 Matches 26; Conservative 18; Mismatches 25; Indels 4; Gaps 2;

OY 13 LRKSR-GFGFTVGGDEP---DEFLQIKSLVDGPALDGMKMTGDIIVSVNDTCVLGH 68  
 DB 1096 LKDDAKYGLGFGIIGERKMRLDGLFISVARGPADLDGCLKPGRLISVSVSLEGV 1155  
 OY 69 THAQVVKIPQSIIP 81  
 DB 1156 SHRAALEILQNP 1168

RESULT 11  
 T10811  
 Channel: associated protein of synapse 2 - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
 C/Accession: T10811  
 R:Irle, M.; Hata, Y.; Takai, Y.  
 submitted to the EMBL Data Library, April 1996  
 A/Description: Cloning of new isoforms of PSD-95/SAP90 related genes.  
 A/Reference number: Z17166  
 A/Cross-references: UNIPROT:Q63622; EMBL:U53368; NID:g1517939; PID:g1517940  
 A/Accession: T10811  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-852 <RI>  
 A/Cross-references: UNIPROT:Q63622; EMBL:U53368; NID:g1517939; PID:g1517940  
 C/Genetics: 8  
 A/Note: PSD-95/SAP90-related gene 2 (chapsyn isoform2)  
 C/Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase hom  
 F:198-276/Domain: GLGF domain homology <GLG>  
 F:543-601/Domain: SH3 homology <SH3>  
 F:663-840/Domain: guanylate kinase homology <GKI>

Query Match 21.9%; Score 115.5; DB 2; Length 852;  
 Best Local Similarity 39.1%; Pred. No. 0.00054;  
 Matches 27; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

OY 4 LKGRFHTHTLRKSSRGFGFTVGGDEPDEFLQIKSLVDGPALDGMKMTGDIIVSVNDT 63  
 DB 415 LRBEPRKVVHLHKSGTGLGFNIIVGG-EDGEGIFVSLIAGGPADLSGELRGDQLISVNGI 473  
 OY 64 CVLGHHTAQ 72  
 DB 474 DLRGASHHQ 482

RESULT 12  
 G01974  
 Channel: associated protein of synapse - human  
 C/Species: Homo sapiens (man)  
 C/Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
 C/Accession: G01974  
 R:Kim, E.; Cho, K.  
 submitted to the EMBL Data Library, July 1995  
 A/Reference number: G08966  
 A/Cross-references: G08966  
 A/Accession: G01974  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-870 <KM>  
 A/Cross-references: UNIPROT:Q15700; EMBL:U32376; NID:g1463025; PID:g1036790  
 C/Genetics: 8  
 A/Gene: Chapsyn-110  
 C/Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase hom  
 F:198-276/Domain: GLGF domain homology <GLG2>  
 F:543-601/Domain: SH3 homology <SH3>  
 F:681-858/Domain: guanylate kinase homology <GKI>

Query Match 21.9%; Score 115.5; DB 2; Length 870;  
 Best Local Similarity 39.1%; Pred. No. 0.00055;  
 Matches 27; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

OY 4 LKGRFHTHTLRKSSRGFGFTVGGDEPDEFLQIKSLVDGPALDGMKMTGDIIVSVNDT 63  
 DB 415 LRBEPRKVVHLHKSGTGLGFNIIVGG-EDGEGIFVSLIAGGPADLSGELRGDQLISVNGI 473  
 OY 64 CVLGHHTAQ 72  
 DB 474 DLRGASHHQ 482

RESULT 13  
 S71625  
 N:Alternative names: epidermal growth factor-binding protein; serine proteinase  
 C/Species: Mus musculus (house mouse)  
 C/Date: 27-Nov-1997 #sequence\_revision 12-Dec-1997 #text\_change 09-Jul-2004  
 C/Accession: S71625; S67987; I81210; I81209; S40290  
 R:Chida, D.; Kume, T.; Mukoyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Watanabe, T.  
 FEBS Lett. 358, 233-239, 1995  
 A/Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very e  
 A/Reference number: S71625; MUID:95145716; PMID:7843407  
 A/Cross-references: S71625  
 A/Molecule type: mRNA  
 A/Residues: 1-2450 <CH1>  
 A/Cross-references: UNIPROT:Q64512; UNIPROT:Q62370; EMBL:D83966; NID:g1232103; PIDN:BA0  
 A/Experimental source: strain DBA/2; cell line MEL 745A  
 R:Wolf, B.B.; Brown, M.D.  
 FEBS Lett. 376, 177-180, 1995  
 A/Title: Epidermal growth factor-binding protein activates soluble and receptor-bound s  
 A/Reference number: S67987; MUID:96105375; PMID:7498536  
 A/Cross-references: S67987  
 A/Molecule type: protein  
 A/Residues: 1098-1102 <MO>  
 A/Experimental source: submaxillary glands  
 R:Sato, T.; Irle, S.; Kitada, S.; Reed, J.C.  
 Science 268, 411-415, 1995  
 A/Title: PAP-1: a protein tyrosine phosphatase that associates with Fas.  
 A/Reference number: 159595; MUID:95232528; PMID:7536343  
 A/Cross-references: 181210  
 A/Accession: 181210  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1329-1354, 'K', 1356-1447, 'R', 1449-1454 <RES>  
 A/Cross-references: GB:L34582; NID:g806297; PIDN:AAC42056.1; PID:g806298  
 A/Accession: 181209  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1338-1354, 'K', 1356-1447, 'R', 1449-1454 <RE2>  
 A/Cross-references: GB:L34581; NID:g806295; PIDN:AAC42055.1; PID:g806296

R,Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
Submitted to the EMBL Data Library, June 1993  
A/Description: Assessment of the expression levels of murine protein-tyrosine phosphatase  
A/Reference number: S40280

A/Accession: S40280  
A/Molecule type: mRNA

A/Residues: 2266-2372 <HEN>

A/Cross-references: EMBL:Z23059; NID:G438155; PIDN:CAAB0594.1; PID:G438156

C/Genetics:

A/Map position: 5

C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;  
C/Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyros  
F/566-860/Domain: protein 4.1 membrane-binding domain homology <B41>  
F/1089-1165/Domain: GLGF domain homology <GLG1>  
F/1361-1437/Domain: GLGF domain homology <GLG2>  
F/1495-1574/Domain: GLGF domain homology <GLG3>  
F/1769-1840/Domain: GLGF domain homology <GLG4>  
F/1863-1937/Domain: GLGF domain homology <GLG5>

F/2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F/2374/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F/2380/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 21.6%; Score 114; DB 2; Length 2450;

Matches 33; Conservative 17; Mismatches 39; Indels 16; Gaps 3;

Y 2 SELKGRITHTKLKRSRGFTVVGDEPDEFLQIKL-----VLDPALDGMKMTGD 55

Db 1756 SELEVEILLITLVSEKSGSLFTVTKGSG-----SIGCVHVIDDPKAGDRLKAGD 1807

Y 56 VIVSVNDTCVLGHTHAQVVKIFOSIPGASVDLELCRGYPLP 100

Db 1808 RLKVNDDVTVMTHTDVAVMLRAAP--KTVRLVGRILEPRMP 1850

RESULT 14

138757

homolog of Drosophila discs large protein, isoform 1 - human

C/Species: Homo sapiens (man)

C/Date: 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C/Accession: 138757

R/Line, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.

Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994

A/Title: Cloning and characterization of hdlg: the human homologue of the Drosophila disc

A/Reference number: 138756; MUID:95024052; PMID:7937897

A/Accession: 138757

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-904 <RES>

A/Cross-references: UNIPROT:Q12959; EMBL:U13897; NID:G558437; PIDN:AAA50599.1; PID:G5584

C/Genetics:

A/Map position: 3q29-3q29

A/Map position: 3q29-3q29

C/Superfamily: discs-large tumor suppressor, GLGF domain homology; guanylate kinase hom

C/Keywords: alternative splicing; duplication

F/229-307/Domain: GLGF domain homology <GLG1>

F/324-402/Domain: GLGF domain homology <GLG2>

F/588-646/Domain: SH3 homology <SH3>

F/715-892/Domain: guanylate kinase homology <GKI>

Query Match

Best Local Similarity 21.3%; Score 112.5; DB 2; Length 904;

Matches 27; Conservative 20; Mismatches 44; Indels 11; Gaps 2;

Y 7 KFIHTKLKRSRGFTVVG-----DEPDEFLQIKSLVLDGPAALDGMKMTGDIYSVN 61

Db 316 KIMEIKLIKPKGKIGFSIAGVGNQHIIPGNSIYVTKIIEGAAHKDGLQIGDKLAVN 375

Y 62 DTCVLGHTHAQVVKI-----FOSIPGASVDLELCRGYPLP 97

Db 376 NVCLIEVTHEAVTALKNTSDFYLVKVAKFTSMYNDGYAP 417

RESULT 15

138756

homolog of Drosophila discs large protein, isoform 2 - human

C/Species: Homo sapiens (man)

C/Date: 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C/Accession: 138756

R/Line, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.

Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994

A/Title: Cloning and characterization of hdlg: the human homologue of the Drosophila di

A/Reference number: 138756; MUID:95024052; PMID:7937897

A/Accession: 138756

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-926 <RES>

A/Cross-references: UNIPROT:Q12959; EMBL:U13896; NID:G558435; PIDN:AAA50598.1; PID:G558

C/Genetics:

A/Map position: 3q29-3q29

A/Map position: 3q29-3q29

C/Superfamily: discs-large tumor suppressor, GLGF domain homology; guanylate kinase hom

C/Keywords: alternative splicing; duplication

F/229-307/Domain: GLGF domain homology <GLG1>

F/324-402/Domain: GLGF domain homology <GLG2>

F/588-646/Domain: SH3 homology <SH3>

F/737-914/Domain: guanylate kinase homology <GKI>

Query Match

Best Local Similarity 21.3%; Score 112.5; DB 2; Length 926;

Matches 27; Conservative 20; Mismatches 44; Indels 11; Gaps 2;

Y 7 KFIHTKLKRSRGFTVVG-----DEPDEFLQIKSLVLDGPAALDGMKMTGDIYSVN 61

Db 316 KIMEIKLIKPKGKIGFSIAGVGNQHIIPGNSIYVTKIIEGAAHKDGLQIGDKLAVN 375

Y 62 DTCVLGHTHAQVVKI-----FOSIPGASVDLELCRGYPLP 97

Db 376 NVCLIEVTHEAVTALKNTSDFYLVKVAKFTSMYNDGYAP 417

Search completed: December 20, 2004, 14:23:00  
Job time : 40 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 20, 2004, 14:09:42 ; Search time 191 Seconds

(without alignments)  
304.256 Million cell updates/sec

Title: US-10-630-590-288

Perfect score: 528

Sequence: 1 PSELKGFHTKLRKSRGF.....IGASVDLECRGYPLPPDP 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_02:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528	100.0	677	2	043863
2	528	100.0	1160	2	096028
3	528	100.0	1171	2	054883
4	528	100.0	1256	2	075085
5	528	100.0	1287	2	096029
6	528	100.0	1462	2	096027
7	528	100.0	1471	2	06RHR9
8	528	100.0	1471	2	AA577818
9	418	79.2	1112	2	AAH59005
10	418	79.2	1252	2	080T00
11	418	79.2	1275	1	AIPI_MOUSE
12	418	79.2	1277	1	AIPI_RAT
13	418	79.2	1455	1	AIPI_HUMAN
14	350	66.3	874	2	09HCD8
15	350	66.3	1074	2	08C088
16	350	66.3	1125	2	09H2V6
17	350	66.3	1126	2	09EQJ9
18	346	65.5	1150	2	09HBC2
19	346	65.5	1179	2	09JKT1
20	331.5	62.8	1202	2	09W212
21	315.5	59.8	1057	2	07Q119
22	242.5	45.9	1012	2	021075
23	182	34.5	308	2	09BWX0
24	164	31.1	1027	2	09HIX7
25	149	28.2	266	2	09CR71
26	149	28.2	266	2	09D9M4
27	136	25.8	157	2	07Q452
28	134	25.4	496	2	08GCP7
29	133.5	25.3	1073	2	08GCP7
30	130	24.6	409	2	09H5Y8
31	129	24.4	97	2	07Q243

32	127.5	24.1	275	2	09H6Y5
33	127.5	24.1	1464	2	096782
34	126.5	24.0	1464	2	09VX75
35	123.5	23.4	747	2	08IX26
36	123.5	23.4	819	2	08IX28
37	123.5	23.4	943	2	08IX27
38	123.5	23.4	1340	2	06IQ47
39	123.5	23.4	1340	2	AAH71566
40	123.5	23.4	1356	1	PAD3_HUMAN
41	122.5	23.2	200	2	09OX35
42	121.5	23.0	721	2	08BP06
43	121.5	23.0	741	2	08BP04
44	121.5	23.0	816	2	09STF5
45	121.5	23.0	911	2	07KV39

## ALIGNMENTS

RESULT 1	ID	043863	PRELIMINARY;	PRT;	677 AA.
AC	043863;				
DT	01-JUN-1998	(TREMBLrel. 06, Created)			
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE	Membrane associated guanylate kinase 1 (Fragment).				
GN	Name=MAGI-1;				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9333405; PubMed=9647693;				
RA	Wood J.D., Yuan J., Margolis R.L., Colomer V., Duan K., Kuehl J.,				
RA	Kaminsky Z., Kleiderlein J.J., Sharp A.H., Rose C.A.;				
RT	"Atrophin-1, the DRP1A gene product, interacts with two families of WW				
RT	domain-containing proteins.";				
RL	Mol. Cell. Neurosci. 11:149-160(1998).				
CC	-1- SIMILARITY: Contains 2 PDZ/DHR domains.				
DR	EMBL; U80754; AAC04844.1; -.				
DR	HSSP; P46937; 1K9R.				
DR	GO; GO:0005911; C:intercellular junction; TAS.				
DR	GO; GO:0005886; C:plasma membrane; TAS.				
DR	GO; GO:0008022; F:protein C-terminus binding; TAS.				
DR	GO; GO:0007155; P:cell adhesion; TAS.				
DR	GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.				
DR	InterPro; IPR008144; Guanylate_kin.				
DR	InterPro; IPR008145; Guanylate_kin.				
DR	InterPro; IPR001478; PDZ.				
DR	InterPro; IPR001202; WW_Reps_WWP.				
DR	Pfam; PF00625; Guanylate_kin; 1.				
DR	Pfam; PF00595; PDZ; 2.				
DR	Pfam; PF00397; WW; 2.				
DR	SMART; SM00072; GUKC; 1.				
DR	SMART; SM00228; PDZ; 2.				
DR	SMART; SM00456; WW; 2.				
DR	PROSITE; PSS0052; GUANYLATE_KINASE_2; 1.				
DR	PROSITE; PSS0106; PDZ; 2.				
DR	PROSITE; PSS0158; WW_DOMAIN_1; 2.				
DR	PROSITE; PSS0020; WW_DOMAIN_2; 2.				
KW	Kinase.				
FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE 677 AA; 74507 MW; 9B4C9EBAAC49D047 CRC64;				

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Query Match          100.0%; Score 528; DB 2; Length 677;
Best Local Similarity 100.0%; Pred. No. 6.7e-46;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60
    |||
Db 314 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 373
    |||

QY 61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 101
    |||
Db 374 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 414
    |||

RESULT 2
Q96QZ8 PRELIMINARY; PRT; 1160 AA.
AC Q96QZ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MAGI-1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laura R.P., Laeky L.A.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 PDZ/DHR domains.
DR EMBL; AF401655; AAK94065.1; -.
DR HSSP; P46937; IK9R.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR008144; Guanylate_kin.
DR InterPro; IPR008145; Guanylt/Ca.
DR InterPro; IPR001202; WW_Reps_WMP.
DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00595; PDZ; 4.
DR SMART; SM00072; GukC; 1.
DR SMART; SM00228; PDZ; 5.
DR SMART; SM00456; WW; 2.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS50106; PDZ; 5.
DR PROSITE; PS01159; WW_DOMAIN_1; 2.
DR PROSITE; PS50020; WW_DOMAIN_2; 2.
SQ SEQUENCE 1160 AA; 126958 MW; 78PE5B621AC295B0 CRC64;

Query Match          100.0%; Score 528; DB 2; Length 1160;
Best Local Similarity 100.0%; Pred. No. 1.2e-45;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60
    |||
Db 463 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 522
    |||

QY 61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 101
    |||
Db 523 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 563
    |||

RESULT 3
OS4893 PRELIMINARY; PRT; 1171 AA.
AC OS4893;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative membrane-associated guanylate kinase 1.
GN Name=Baiapl; Synonyms=Magi-1;

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57 Black/6 x CBA;
RA Dobrosotckaya I.; Guy R.K., James G.L.;
RT "MAGI-1: A Membrane-Associated Guanylate Kinase with a Unique
RT Arrangement of Protein-Protein Interaction Domains.";
RL J. Biol. Chem. 0:0-0(1997).
CC -1- SIMILARITY: Contains 4 PDZ/DHR domains.
DR EMBL; AF027503; AAB91995.1; -.
DR PIR; T42372; T42372.
DR HSSP; P46937; IK9R.
DR WGD; MG1:1203522; Baiapl.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR008144; Guanylate_kin.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001202; WW_Reps_WMP.
DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00595; PDZ; 4.
DR SMART; SM00072; GukC; 1.
DR SMART; SM00228; PDZ; 5.
DR SMART; SM00456; WW; 2.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS50106; PDZ; 5.
DR PROSITE; PS01159; WW_DOMAIN_1; 2.
DR PROSITE; PS50020; WW_DOMAIN_2; 2.
SQ SEQUENCE 1171 AA; 127522 MW; FC793D6640D3959 CRC64;

Query Match          100.0%; Score 528; DB 2; Length 1171;
Best Local Similarity 100.0%; Pred. No. 1.2e-45;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60
    |||
Db 443 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 502
    |||

QY 61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 101
    |||
Db 503 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 543
    |||

RESULT 4
O75085 PRELIMINARY; PRT; 1256 AA.
ID O75085;
AC O75085;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BA11-associated protein 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=98321173; PubMed=9647739;
RA Shiratsuchi T., Futamura M., Oda K., Nishimori H., Nakamura Y.,
RA Tokino T.;
RT "Cloning and characterization of BA1-associated protein 1: a PDZ domain-
RT containing protein that interacts with BA11.";
RL Biochem. Biophys. Res. Commun. 247:597-604(1998).
CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.
DR EMBL; AB010894; BAA32002.1; -.
DR PIR; J60209; J60209.

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DR HSSP; P46937; 1K9R.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR InterPro; IPR008144; Guanylate\_kin.  
 DR InterPro; IPR008145; Guanylate\_kin.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR001202; WW\_Reps\_WMP.  
 DR Pfam; PF00625; Guanylate\_kin; 1.  
 DR Pfam; PF00595; PDZ; 5.  
 DR Pfam; PF00397; WW; 2.  
 DR SMART; SM00072; Gukc; 1.  
 DR SMART; SM00228; PDZ; 6.  
 DR SMART; SM00456; WW; 2.  
 DR PROSITE; PS00856; GUANYLATE\_KINASE\_1; 1.  
 DR PROSITE; PS50052; GUANYLATE\_KINASE\_2; 1.  
 DR PROSITE; PS50106; PDZ; 6.  
 DR PROSITE; PS01159; WW\_DOMAIN\_1; 2.  
 DR PROSITE; PS50020; WW\_DOMAIN\_2; 2.  
 DR PROSITE; PS50020; WW\_DOMAIN\_2; 2.  
 SQ SEQUENCE 1256 AA; 83PAD2091A4C8E4 CRC64;

Query Match 100.0%; Score 528; DB 2; Length 1256;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-45;  
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMKMTGDIIVSV 60  
 DB 463 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMKMTGDIIVSV 522  
 QY 61 NDTCVLGHTHAQQVKIFQSIPIGASVDLELCRGYPLPFDDP 101  
 DB 523 NDTCVLGHTHAQQVKIFQSIPIGASVDLELCRGYPLPFDDP 563

## RESULT 5

Q96QZ9 PRELIMINARY; PRT; 1287 AA.  
 AC Q96QZ9; 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE MAGI-1B alpha beta.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Laura R.P., Laeky L.A.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.  
 DR EMBL; AF401654; AKR94064.1; -.  
 DR HSSP; P46937; 1K9R.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR InterPro; IPR008144; Guanylate\_kin.  
 DR InterPro; IPR008145; Guanylate\_kin.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR001202; WW\_Reps\_WMP.  
 DR Pfam; PF00625; Guanylate\_kin; 1.  
 DR Pfam; PF00595; PDZ; 5.  
 DR Pfam; PF00397; WW; 2.  
 DR SMART; SM00072; Gukc; 1.  
 DR SMART; SM00228; PDZ; 6.  
 DR SMART; SM00456; WW; 2.  
 DR PROSITE; PS00856; GUANYLATE\_KINASE\_1; 1.  
 DR PROSITE; PS50052; GUANYLATE\_KINASE\_2; 1.  
 DR PROSITE; PS50106; PDZ; 6.  
 DR PROSITE; PS01159; WW\_DOMAIN\_1; 2.  
 DR PROSITE; PS50020; WW\_DOMAIN\_2; 2.  
 SQ SEQUENCE 1287 AA; 140438 MW; C676655657BD5D5 CRC64;

Query Match 100.0%; Score 528; DB 2; Length 1287;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-45;  
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMKMTGDIIVSV 60  
 DB 463 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMKMTGDIIVSV 522  
 QY 61 NDTCVLGHTHAQQVKIFQSIPIGASVDLELCRGYPLPFDDP 101  
 DB 523 NDTCVLGHTHAQQVKIFQSIPIGASVDLELCRGYPLPFDDP 563

## RESULT 6

Q96QZ7 PRELIMINARY; PRT; 1462 AA.  
 AC Q96QZ7; 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE MAGI-1C beta.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Laura R.P., Laeky L.A.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.  
 DR EMBL; AF401656; AKR94066.1; -.  
 DR PIR; J0209; J0209.  
 DR HSSP; P46937; 1K9R.  
 DR Genew; HGNC:946; BA1A1.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR InterPro; IPR008144; Guanylate\_kin.  
 DR InterPro; IPR008145; Guanylate\_kin.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR001202; WW\_Reps\_WMP.  
 DR Pfam; PF00625; Guanylate\_kin; 1.  
 DR Pfam; PF00595; PDZ; 5.  
 DR Pfam; PF00397; WW; 2.  
 DR SMART; SM00072; Gukc; 1.  
 DR SMART; SM00228; PDZ; 6.  
 DR SMART; SM00456; WW; 2.  
 DR PROSITE; PS00856; GUANYLATE\_KINASE\_1; 1.  
 DR PROSITE; PS50052; GUANYLATE\_KINASE\_2; 1.  
 DR PROSITE; PS50106; PDZ; 6.  
 DR PROSITE; PS01159; WW\_DOMAIN\_1; 2.  
 DR PROSITE; PS50020; WW\_DOMAIN\_2; 2.  
 SQ SEQUENCE 1462 AA; 161609 MW; 2B98A448A9E7DF89 CRC64;

Query Match 100.0%; Score 528; DB 2; Length 1462;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-45;  
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMKMTGDIIVSV 60  
 DB 463 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMKMTGDIIVSV 522  
 QY 61 NDTCVLGHTHAQQVKIFQSIPIGASVDLELCRGYPLPFDDP 101  
 DB 523 NDTCVLGHTHAQQVKIFQSIPIGASVDLELCRGYPLPFDDP 563

## RESULT 7

Q6RHR9 PRELIMINARY; PRT; 1471 AA.  
 AC Q6RHR9; 05-JUL-2004 (Tremblrel. 27, Created)  
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
 DE MAGI1C alpha beta2 gamma.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=129/SVHe; TISSUE=Brain endothelium;  
RA Wegmann F., Ebnet K., Du Pasquier L., Vestweber D., Butz S.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.  
DR EMBL: AY497557; AAS77818.1; --  
DR InterPro: IPR008144; Guanylate\_kin.  
DR InterPro: IPR008145; Guanylc/Ca.  
DR InterPro: IPR001202; WW\_Reps\_WWP.  
DR Pfam: PF00625; Guanylate\_kin; 1.  
DR Pfam: PF00595; PDZ; 5.  
DR Pfam: PF00397; WW; 2.  
DR SMART: SM00072; GUKC; 1.  
DR SMART: SM00228; PDZ; 6.  
DR SMART: SM00456; WW; 2.  
DR PROSITE: PS00856; GUANYLATE\_KINASE\_1; 1.  
DR PROSITE: PS0052; GUANYLATE\_KINASE\_2; 1.  
DR PROSITE: PS0106; PDZ; 6.  
DR PROSITE: PS0159; WW\_DOMAIN\_1; 2.  
DR PROSITE: PS0020; WW\_DOMAIN\_2; 2.  
DR PROSITE: PS0020; WW\_DOMAIN\_2; 2.  
SQ SEQUENCE 1471 AA; 161973 MW; 6C780C71CAC37CB1 CRC64;

Query Match 100.0%; Score 528; DB 2; Length 1471;  
Best Local Similarity 100.0%; Pred. No. 1,6e-45;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PSELKGFHTKLRKSSRGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 60  
DB 455 PSELKGFHTKLRKSSRGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 514  
QY 61 NDTCVLGHTHAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 101  
DB 515 NDTCVLGHTHAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 555

RESULT 8  
AAS77818 PRELIMINARY; PRT; 1471 AA.  
AC AAS77818;  
DT 10-MAY-2004 (TrEMBLrel. 27, Created)  
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)  
DT 10-MAY-2004 (TrEMBLrel. 27, Last annotation update)  
DE MAGIC alpha beta2 gamma.  
GN MAGI.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SVHe; TISSUE=Brain endothelium;  
RA Wegmann F., Ebnet K., Du Pasquier L., Vestweber D., Butz S.;  
RL "Endothelial adhesion molecule ESAM binds directly to the multidomain  
RT adaptor MAGI-1 and recruits it to cell contacts."  
Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY497557; AAS77818.1; --  
SQ SEQUENCE 1471 AA; 161973 MW; 6C780C71CAC37CB1 CRC64;

Query Match 100.0%; Score 528; DB 2; Length 1471;  
Best Local Similarity 100.0%; Pred. No. 1,6e-45;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PSELKGFHTKLRKSSRGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 60  
DB 455 PSELKGFHTKLRKSSRGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 514  
QY 61 NDTCVLGHTHAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 101  
DB 515 NDTCVLGHTHAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 555

RESULT 9  
AAH59005 PRELIMINARY; PRT; 1112 AA.  
ID AAH59005  
AC AAH59005;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Actin receptor interacting protein 1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=2238257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedl T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Gilmour J., Schmidt J., Myers R.M., Butterfield Y.S.,  
RA Krzywnicki M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Maier W.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC059005; AAH59005.1; --  
KW Receptor.  
SQ SEQUENCE 1112 AA; 122598 MW; 7B782082930C8490 CRC64;

Query Match 79.2%; Score 418; DB 2; Length 1112;  
Best Local Similarity 74.0%; Pred. No. 2,8e-34;  
Matches 74; Conservative 15; Mismatches 11; Indels 0; Gaps 0;  
QY 2 SELKGFHTKLRKSSRGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 61  
DB 254 SQLKGFHTKLRKSSRGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 313  
QY 62 DTCVGLGHTHAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 101  
DB 314 EYCVLGHTHAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 353

RESULT 10  
O80TU0 PRELIMINARY; PRT; 1252 AA.  
ID O80TU0  
AC O80TU0;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE MKIAA0705 protein (Fragment).  
GN Name=Acvripl; Synonyms=mkIAA0705;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22579291; PubMed=12693553;  
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,  
 RA Nakajima D., Nagase T., Ohara O., Koga H.,  
 RT "Prediction of the coding nucleotide sequences of 400 mouse homologues of KIAA gene:  
 RT 1. The complete nucleotide sequences of 400 mouse KIAA-homologous  
 RT cDNAs identified by screening of terminal sequences of cDNA clones  
 RT randomly sampled from size-fractionated libraries.";  
 RL DNA Res. 10:35-48(2003).  
 CC -1- SIMILARITY: Contains 5 PDZ/DIR domains.  
 DR EMBL; AK122349; BAC65631.3;  
 DR MGI; MGI:1354953; Acvripl.  
 DR GO; GO:0004871; F:signal transducer activity; IPI.  
 DR GO; GO:0007165; P:signal transduction; IPI.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR001202; WW\_Reps\_WWP.  
 DR Pfam; PF00397; WW; 2.  
 DR Pfam; PF00397; WW; 2.  
 DR SMART; SM00072; GUKC; 1.  
 DR SMART; SM00228; PDZ; 5.  
 DR SMART; SM00456; WW; 2.  
 DR PROSITE; PS0106; PDZ; 5.  
 DR PROSITE; PS01159; WW\_DOMAIN\_1; 2.  
 DR PROSITE; PS0020; WW\_DOMAIN\_2; 2.  
 FT NON TER 1  
 SQ SEQUENCE 1252 AA; 137278 MW; 3D17EBF5918FDC29 CRC64;  
 Query Match 79.2%; Score 418; DB 2; Length 1252;  
 Best Local Similarity 74.0%; Pred. No. 3.2e-34;  
 Matches 74; Conservative 15; Mismatches 11; Indels 0; Gaps 0;  
 QY 2 SELKGRIRHKLKSSRGFGTVVGGDEPPEFLQIKSLVLDGPALDGKRETVIYSVN 61  
 DB 263 SOLKGLSTLTKKSNMGFTIIGDPEFLQVKSTIPDGPAAODGKMETGVIIYIN 322  
 QY 62 DTCVLGHTAOVYKIFOSIPFGASVDELRCRGYLPDPDP 101  
 DB 323 EVCVLGHTADVYKLFOSVPIGOSVNLVLCRGYLPDPDP 362  
 RESULT 11  
 AIP1\_MOUSE STANDARD; PRT: 1275 AA.  
 AC Q9WVQ1; Q8BYT1; Q8CA85;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Atrophin-1 interacting protein 1 (Membrane associated guanylate kinase  
 DE inverted-2) (MGI-2) (Activin receptor interacting protein 1)  
 DE (Acvripl).  
 GN Name=AIP1; Synonyms=Magi2, Atp1, Acvripl;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), INTERACTION WITH MADH2; MADH3  
 RP AND ACVR2, AND IDENTIFICATION IN A COMPLEX WITH ACVR2; ACVR1B AND  
 RP MADH3.  
 RC STRAIN=ICR; TISSUE=Brain;  
 RX MEDLINE=20148748; PubMed=10681527;  
 RA Shoji H., Tsuchida K., Kishi H., Yamakawa N., Matsuzaki T., Liu Z.,  
 RA Nakamura T., Sugino H.,  
 RT "Identification and characterization of a PDZ protein that interacts  
 RT with activin types II receptors.";  
 RL J. Biol. Chem. 275:5485-5492(2000).  
 RP [2]  
 RP SEQUENCE OF 159-112 FROM N.A. (ISOFORM 3).  
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus, and Spinal cord;  
 RX MEDLINE=2354683; PubMed=1246851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Oseko N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schobach C., Gotohori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirral L.M., Kanapin A., Matsumoto H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Bruch V., Chochia K., Corbani L.E., Cousins S.,  
 RA Datta E., Dragan T.A., Fletcher C.F., Forrest A., Fraser K.S.,  
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,  
 RA Grimmer S., Guellinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Maki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imocant K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yaenunshi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 CC -1- FUNCTION: Seems to act as scaffold molecule at synaptic junctions  
 CC by assembling neurotransmitter receptors and cell adhesion  
 CC proteins. May play a role in regulating activin-mediated signaling  
 CC in neuronal cells. Enhances the ability of PREN to suppress ACT1  
 CC activation (By similarity).  
 CC -1- SUBUNIT: Interacts via its WW domains with DRPLA (By similarity).  
 CC Interacts via its second PDZ domain with PREN unphosphorylated C-  
 CC terminus (By similarity). Interacts through its guanylate kinase  
 CC domain with DLGAP1 (By similarity). Interacts through the PDZ  
 CC domains with GRIN2A, GRIN2B and NLGN1 (By similarity). Interacts  
 CC with CTNND2, CTNNA1 and MAGUIN-1 (By similarity). Interacts with  
 CC ACVR2, MADH2 and MADH3. Part of a complex consisting of AIP1,  
 CC ACVR2, ACVR1B and MADH3.  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated in synapsesomes (By  
 CC similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1; Synonyms=long;  
 CC IsoId=Q9WVQ1-1; Sequence=Displayed;  
 CC Name=2; Synonyms=short;  
 CC IsoId=Q9WVQ1-2; Sequence=VSP\_008436;  
 CC Note=Major;  
 CC Name=3;  
 CC IsoId=Q9WVQ1-3; Sequence=VSP\_008437;  
 CC Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: Specifically expressed in brain.  
 CC -1- SIMILARITY: Belongs to the MAGUK family.  
 CC -1- SIMILARITY: Contains 1 guanylate kinase-like domain.  
 CC -1- SIMILARITY: Contains 6 PDZ/DIR domains.  
 CC -1- CAUTION: Ref.2 (BAC29987) sequence differs from that shown due to  
 CC a frameshift in position 102.  
 CC -----  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC DR EMBL; AB029485; BAC82294.1;  
 CC DR EMBL; AK039336; BAC30321.1; ALT INIT.  
 CC DR EMBL; AK038407; BAC29987.1; ALT\_FRAME.  
 CC DR PIR; P10546; P10698.



DR InterPro: IPR001478; PDZ.  
DR InterPro: IPR001478; WW\_Rsp5\_WMP.  
DR Pfam: PF00625; Guanylate\_kin1.  
DR Pfam: PF00595; PDZ; 6.  
DR Pfam: PF00397; WW; 2.  
DR SMART: SMO0072; GucK; 1.  
DR SMART: SMO0228; PDZ; 6.  
DR SMART: SMO0456; WW; 2.  
DR PROSITE: PS00856; GUANYLATE\_KINASE\_1; 1.  
DR PROSITE: PS00502; GUANYLATE\_KINASE\_2; 1.  
DR PROSITE: PS0106; PDZ; 6.  
DR PROSITE: PS01159; WW\_DOMAIN\_1; 2.  
DR PROSITE: PS0020; WW\_DOMAIN\_2; 2.  
KW Alternative splicing; Repeat.  
FT DOMAIN 17 101 PDZ.  
FT DOMAIN 109 285 Guanylate\_kinase.  
FT DOMAIN 302 335 WW 1.  
FT DOMAIN 348 381 WW 2.  
FT DOMAIN 426 510 PDZ 1.  
FT DOMAIN 605 683 PDZ 2.  
FT DOMAIN 778 860 PDZ 3.  
FT DOMAIN 920 1010 PDZ 4.  
FT DOMAIN 1141 1223 PDZ 5.  
FT VARSPLIC 1 163 Missing (in isoform 2).  
FT VARSPLIC 1 223 /FTID=VSP\_008438.  
FT FT FT FT Missing (in isoform 3).  
FT FT FT FT /FTID=VSP\_008439.  
FT FT FT FT L -> F (in Ref. 2).  
SQ SEQUENCE 1277 AA; 141071 MW; E1A435FP35549DF9 CRC64;  
  
Query Match 79.2%; Score 418; DB 1; Length 1277;  
Beat Local Similarity 74.0%; Pred. No. 3.3e-34;  
Matches 74; Conservative 15; Mismatches 11; Indels 0; Gaps 0;  
  
QY 2 SELKGRFHTTKLRKSRGFGFTVWGDPDEPLQIKSLVLDGPALDGMETGDIYSVN 61  
Db 418 SQLKGTFLSTLTKSKSMGFGFTIIGSDPDEPLQVKSYPIDGPAQDGKMETGDIYVIN 477  
  
QY 62 DTCVLGHTHAQVVKIFQSGIPICASVDLELCRGYPPLPPDP 101  
Db 478 EVCVLGHTHADVVKLFQSGVPIGQSVNLVLCRGYPPLPPDE 517  
  
RESULT 13  
AIP1\_HUMAN STANDARD; PRT; 1455 AA.  
ID AIP1\_HUMAN  
AC 086CUL; 060434; 060510; 086U1; Q9UD05; Q9UDU1;  
DC 10-OCT-2003 (Rel. 42; Created)  
DT 10-OCT-2003 (Rel. 42; Last sequence update)  
DT 01-OCT-2004 (Rel. 45; Last annotation update)  
DE Atrophin-1 interacting protein 1 (Atrophin-1 interacting protein A)  
DE (Membrane associated guanylate kinase inverted-2) (MAGI-2).  
GN Name=AIP1; Synonyms=MAGI2, KIAA0705;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND INTERACTION  
RC WITH DRPLA.  
RC TISSUE=Brain;  
RX MEDLINE=98313405; PubMed=9647693;  
RX Wood J.D., Yuan J., Margolis R.L., Colomer V., Duan K., Kushi J.,  
RX Kaminsky Z., Kleiderlein J.J., Sharp A.H., Rose C.A.;  
RT "Atrophin-1, the DRPLA gene product, interacts with two families of WW  
RT domain-containing proteins.";  
RL Mol. Cell. Neurosci. 11:149-160 (1998).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Brain;  
RX MEDLINE=98403880; PubMed=9734811;  
RX Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,  
RX Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.  
RT The complete sequences of 100 new cDNA clones from brain which can  
RT code for large proteins in vitro.";  
RL DNA Reel. 5:169-176(1998).  
RN [3]  
RP SEQUENCE OF 1-100; 141-179; 350-682; 684-1175 AND 1237-1455 FROM N.A.  
RA Courtney L., Harrison M., Lemox S., Bourne S., Osercky P., Carter T.,  
RA Tin-Moliam A., Hawkins M., Keppeler D., Sulston J.E., Eldred J.,  
RA Kozlowski A., Benis G., Langeon Y., Mead K., Haakenson W., Meyer R.,  
RA Shih K., Waterston R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION WITH PTEN.  
RX MEDLINE=202226087; Pubmed=10760291;  
RA Wu X., Hepler K., Castellino-Prabhu S., Do D., Kaye M.B., Yuan X.-J.,  
RA Wood J., Ross C., Sawyers C.L., Whang Y.E.;  
RT "Evidence for regulation of the PTEN tumor suppressor by a membrane-  
RT localized multi-PDZ domain containing scaffold protein MAGI-2",  
RL Proc. Natl. Acad. Sci. U.S.A. 97:4233-4238(2000).  
RN [5]  
RP INTERACTION WITH PTEN.  
RX MEDLINE=21623681; Pubmed=11707429; DOI=10.1074/jbc.C100556200;  
RA Vazquez F., Grossman S.R., Takahashi Y., Rokas M.V., Nakamura N.,  
RA Sellers W.R.;  
RT "Phosphorylation of the PTEN tail acts as an inhibitory switch by  
RT preventing its recruitment into a protein complex.";  
RL J. Biol. Chem. 276:48627-48630(2001).  
CC -1- FUNCTION: Seems to act as scaffold molecule at synaptic junctions  
CC by assembling neurotransmitter receptors and cell adhesion  
CC proteins. May play a role in regulating activin-mediated signaling  
CC in neuronal cells. Enhances the ability of PTEN to suppress Akt1  
CC activation.  
CC -1- SUBUNIT: Interacts via its WW domains with DRPLA. Interacts via  
CC its second PDZ domain with PTEN unphosphorylated C-terminus.  
CC Interacts through its guanylate kinase domain with DGAP1 (By  
CC similarity). Interacts through the PDZ domain with GRIN2A, GRIN2  
CC and NIGM1 (By similarity). Interacts with CTNND2, CTNNB1, MAGUIN-  
CC 1, ACVR2, MADH2 and MADH3 (By similarity). Part of a complex  
CC consisting of AIP1, ACVR2, ACVR1B and MADH3 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Membrane-associated in synaptosomes (By  
CC similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q86UL8-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q86UL8-2; Sequence=VSP\_008435;  
CC Note=No experimental confirmation available;  
CC -1- TISSUE SPECIFICITY: Specifically expressed in brain.  
CC -1- SIMILARITY: Belongs to the MAGUK family.  
CC -1- SIMILARITY: Contains 1 guanylate kinase-like domain.  
CC -1- SIMILARITY: Contains 6 PDZ/DHR domains.  
CC -1- SIMILARITY: Contains 2 WW domains.  
CC -----  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
DR EMBL; AF038563; AAC05370.1; -;  
DR EMBL; AB014605; BAA31680.2; ALT\_INIT.  
DR EMBL; AC004808; AAC23438.1; -;  
DR EMBL; AC004945; AAC61488.1; -;  
DR EMBL; AC004990; AAC79151.1; -;  
DR EMBL; AC005246; AAC25530.1; -;  
DR EMBL; AC006043; AAD15413.2; -;  
DR EMBL; AC071200; AAP22360.1; -;  
DR EMBL; AC007237; AAP21886.1; -;  
DR PDB; 1UEP; NMR; A=768-873.  
DR PDB; 1UEP; NMR; A=405-528.

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20450683; PubMed=10997877;  
 RA Nagase T., Kikuno R., Nakayama M., Hiroseawa M., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes.  
 RT XVII. The complete sequences of 100 new cDNA clones from brain which  
 RT code for large proteins in vitro."  
 RL DNA Res. 7:273-281(2000).  
 CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.  
 DR EMBL; AB046854; BAB13460.1; -  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR001202; WW\_Rsp5\_WMP.  
 DR Pfam; PF00595; PDZ; 5.  
 DR Pfam; PF00397; WW; 2.  
 DR SMART; SM00228; PDZ; 5.  
 DR SMART; SM00456; WW; 2.  
 DR PROSITE; PSS0106; PDZ; 5.  
 DR PROSITE; PSS0159; WW\_DOMAIN 1; 2.  
 DR PROSITE; PSS0020; WW\_DOMAIN 2; 2.  
 FT NON TER 1  
 FT SEQUENCE 874 AA; 95522 MW; 32CBDD7CE59838A CRC64;  
 SO  
 Query Match 66.3%; Score 350; DB 2; Length 874;  
 Best Local Similarity 60.4%; Pred. No. 2, 4e-27;  
 Matches 61; Conservative 18; Mismatches 22; Indels 0; Gaps 0  
 Oy 1 PSELKGFHTTKRKSSRQFGTTVVGDEDFLOIKSLVLDGPALDGRKETGVIVSV 60  
 Db 150 PSQIKGLVRLASIKSTWGFETITIGCRPDFFLQVKVNLXDPAPAOGKIAIPGVYDI 209  
 Oy 61 NDTCVLGHHTAQAQVVKIFQSIPIGASVDELTCGYPELPPDD 101  
 Db 210 NGNCVLGHTHADVQGMQLVPAVQVYVNLTCRGYFLPDDSE 250  
 RESULT 15  
 O8COP8 PRELIMINARY; PRT; 1074 AA.  
 AC O8COP8;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
 DE library, clone:4932436K10 product:MEMBRANE-ASSOCIATED GUANYLATE  
 DE KINASE-RELATED MAGI-3 homolog (Fragment).  
 GN Name=6530407C02Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning."  
 RT Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RT Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RA The FANTOM Consortium;  
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RT Nature 420:563-571(2002).  
 RL

RN [4] SEQUENCE FROM N. A.  
 RP STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-triappor-selected cDNAs to  
 RL prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RN Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N. A.  
 RP STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20530913; PubMed=11076661;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama Y., Nishi K., Kitaura T., Teshiro H., Itoh M.,  
 RA Suni N., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RN Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N. A.  
 RP STRAIN=C57BL/6J; TISSUE=Testis;  
 RA Adechi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Furukawa S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Iehi Y., Itoh M., Kagawa I., Kaikawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsumura T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nihi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JULY-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 4 PDZ/DHR domains.  
 CC EMBL; AK030063; BAC26773.1; -  
 DR HSP, P46937.1K9.  
 DR MGSP; MGI:1923484; 6530407C02R1K.  
 DR GO; GO:0016301; P:kinase activity; IEA.  
 DR GO; GO:0005515; P:protein binding; IEA.  
 DR InterPro; IPR008144; Guanylate kin.  
 DR InterPro; IPR009145; Guanylyl/Ca.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR001202; WW\_Rsp5\_WWP.  
 DR Pfam; PF00625; Guanylate\_kin; 1.  
 DR Pfam; PF00595; PDZ; 4.  
 DR Pfam; PF00397; WW; 2.  
 DR SMART; SM00072; GUKC; 1.  
 DR SMART; SM00228; PDZ; 6.  
 DR SMART; SM00456; WW; 2.  
 DR PROSITE; PS00856; GUANYLYLATE\_KINASE\_1; 1.  
 DR PROSITE; PS50052; GUANYLYLATE\_KINASE\_2; 1.  
 DR PROSITE; PS50106; PDZ; 6.  
 DR PROSITE; PS01159; WW\_DOMAIN\_1; 2.  
 DR PROSITE; PS50020; WW\_DOMAIN\_2; 2.  
 KW Kinase.  
 PT NON TER 1 1  
 SQ SEQUENCE 1074 AA; 117623 MW; 72B32E37D00382E4 CRC64;

Query Match	66.3%	Score 350;	DB 2;	Length 1074;
Best Local Similarity	60.4%	Pred. No. 3e-27;		
Matches	61;	Conservative 18;	Mismatches 22;	Indels 0;
			Gaps	0

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QY      1 PSELKGRKIHRLKSSSGFGFTVVGSGBPDEFLIKSLVLDGPAALGKHETGVIYSV 60
Db      352 PSQLGVGLVRASLKKSTWGFGFTIIIGSGRPDEFVLQVKKDKGPAADGKIAPGDIVDI 411
QY      61 NDTCVLGHTHAQVVKIPQSIPIGASVDELCEGYLPDPDP 101

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Db 412 NGNCVLSGHTHADVYQMFLVPVNGYNNLTLCRGYPLPDDSE 452

Search completed: December 20, 2004, 14:22:18  
Job time : 195 secs

